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February 27, 2002, 11:41:13 ; Search time 303.5 Seconds
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GenCore vérsion 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES			01	AAR94470	AAR94473	AAR94476	AAR94468	AAR94477	AAR94475	AAR94474	AAR94482	AAR94478	AAR94479	AAW27250
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	œ	Ouery	Match	98.0	98.0	96.0	96.0	94.0	88.0	86.0	86.0	84.0	84.0	84.0
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Molecular adjuvant Molecular adjuvant CSa anaphylatoxin CSa analogue CSa(6 CSa anaphylatoxin CSa anaphylatoxin CSa anaphylatoxin CSa anaphylatoxin	C5a anaphylatoxin C5a anaphylatoxin C5a anaphylatoxin C5a anaphylatoxin Human lymphoid-spe C5a anaphylatoxin Control decapeptid Human C5a anaphyla C5a anaphylatoxin Staphylococcus aur Staphylococcus aur Staphylococcus aur Hexose oxidase, an Synthetic hexose o	ALIGNMENTS 10 AA. analogue C5a(65-74) Tyr65 Ala73. ylatoxin; analogue; beta-turn; ation; proinflammatory response; agaion; neutrophil; non-mediated; orane; vascular; permeability;	neutrophil polarisation; neutrophil enzyma release; treadment; immune adjuvant; immunodeficiecy; augmentation; immune therapy; cancer; drug delivery. CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory. Homo sapiens. Location/Qualifiers Region Anote= "beta-turn" WO9606629-Al. 07-MAR-1996. 31-AUG-1994; 95WO-USI1126.
AAW27254 AAW27255 AAW27251 AAW3489 AAR94490 AAR94493 AAR94495 AAR94495 AAR94495 AAR94496 AAR94496 AAR94496 AAR94496 AAR94489	44465 44472 7237 7237 7238 7238 7238 7239 7239 7339 7339 7339 7339 7339 7339	ALIGNMENT AA. AA. alogue C5 con; proin; an tion; neu	nil en dr; aug dr; aug dr; aug in affi infla in aug
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. 4444444444444444444444444444444444444	4 W W W W W W W W W W W W W W W W W W W	AAR94470 standard; peptide; AAR94470: 17-OCT-1996 (first entry) C5a anaphylatoxin C-termina C-terminal; human; C5a anap constrained hackbone confor spasmogenesis; platelet aga	neutrophil po cimmune adjuva cancer: drug Alzheimer's d development; Homo sapiens. Key Region WO9606629-Al. 07-MAR-1996. 31-AUG-1994;
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Thu Feb 28 09:50:25 2002

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                                                                                                                                                                                                                                                                     region from human C5a anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with type C11 or V) and type III beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (sep.
                                                                                                                                  C-terminal analogues of C5a anaphylatoxin · induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                            The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affinity CSa receptor antagonists useful as non-steroidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In a type (II or V) beta-turn specific human foetal artery smooth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle contraction assay, and a type III beta turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of 122 and 48, compared to 0.018 and 0.0013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constrained backbone conformation; proinflammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated; mediated; increase; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment;
                                                                                                                                                                                                                                                     The present peptide is an analogue of a C-terminal decapeptide
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                                                            Taylor SM;
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                                                            Sherman SA,
                                                                                                                                                                                                                                                                                                                                                                                                                               vascular) permeability, respectively.
                                                                                                                                                                                                            Example:2; Page 79; 116pp; English.
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90.0%;
                                                          Sanderson DG,
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Matches 9; Conservative
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  NEBRASKA.
QUEENSLAND
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                                                          Kirnarsky L,
(UYNE-) UNIV
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Gaps
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The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune effects. They can also be used to facilitate drug delivery by
                                                                                                                                                                                                                                                                                                                                  C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      In a type (II or V) beta-turn specific human foetal artery smooth muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microm) activities of 0.35 and 2.1, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or Lumours, and to develop high affinity CSa receptor antagonists useful as non-steroidal anti-inflammatory agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.0%; Score 49; DB 17; Length 10; 90.0%; Pred. No. 0.0013; ive 0; Mismatches 1; Indels
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                                /note= "D-form residue"
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/note= "beta-turn"
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                                                                                                                                      95WO-US11126.
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              Misc-difference
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Location/Qualifiers

Region

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us-09-446-109a-3.rag

constrained backbone conformation; proinflammatory response. Spasmogenesis; platelet aggregation; neutrophil; non-mediated; necrease; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; drug dellivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.

Location/Qualifiers /note= "beta-turn"

HOMO Sapiens

C5a anaphylatoxin C-terminal analogue C5a(65-74) Tyr65 Pro71.

(first entry)

17-0CT-1996

AAR94468;

AAR94468 standard; peptide; 10 AA

AAR94468

C-terminal; human; C5a anaphylatoxin; analogue; beta-turn;

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The present peptide is an analogue of a C-terminal decapeptide region from human C5a anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with type (II or V) and type III beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil elease and neutrophil mediated increases in cell membrane (esp. vascular) permeability, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-terminal analogues of C5a anaphylatoxin - induce e.g.
spasmogenesis, platelet aggregation and increases in cell membrane
permeabllity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In a type (II or'v) beta-turn specific human foetal artery smooth muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microm) activities of 51.1 and 4.0, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal
spasmoyenesis; platelet aggregation; neutrophil; non-mediated; mediated; increase; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immunodeficiency; augmentation; immune therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzhelmer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
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                                                                                                                                                                                                                                                                         /note= "D-form residue"
                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                /note= "beta-turn"
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                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       31-AUG-1995;
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The present peptide is an analogue of a C-terminal decapeptide region from human C5a anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with type (II or V) and type III beta-turns elicit proinf: ...matory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (esp. vascular) permeability, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affinity CSa receptor antagonists useful as non-steroidal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscle contraction assay, and a type fII beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of 1.13 and 5, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-inflammatory agents.
In a type (11 or V) beta-turn specific human foetal artery
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1.0 AA;

Sequence

.; 0

Gaps

.; 0

Score 48; DB 17; Length 10; Pred. No. 0.0021; 0; Mismatches 1; Indels

96.08;

Best Local Similarity 90.0 Matches 9; Conservative

Query Match

1 YSFKDMPLXR 10

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C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increasus in cell membrane

Taylor SM;

Sherman SA,

Sanderson DG,

Kirnarsky L,

WPI; 1996-160140/16.

permeability

UNIV QUEENSLAND. (UYNE-) UNIV NEBRASKA

(UYQU

94US-0299285 95WO-US11126

31-AUG-1994;

31-AUG-1995;

07-MAR-1996

WO9606629-A1

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                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
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                                                                                                                                                                                                                                                                                                                  C-terminal: human; C5a anaphylatoxin; analogue; beta-turn; constrained backbone conformation; proinflammator "response; spasmogenesis; platelet aggregation; neutrophil; non-mediated; merdated; increase; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The analogues can be used as immune adjuvants for the treatment immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     effects. They can also be used to facilitate drug delivery by
                                                                                                                                                                                                                                                                                     C5a anaphylatoxin analogue C5a(65-74) Tyr65 Pro71 D-Pro73.
   Length 10;
                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taylor SM;
   DB 17;
 Score 48; DB 17;
Pred. No. 0.0021;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note- "beta-turn"
                                                                                                                                                                                 AAR94477-standard; peptide; 10 AA.
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 96.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanderson DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95WO-US11126
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                                                                                                                                                                                                                                                     (first entry)
Ouery Match 96.0
Best Local Similarity 90.0
Matches 9; Conservative
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(UYQU ) UNIV QUEENSLAND.
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                                                                  1 YSFKDMPLXR 10
                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kirnarsky L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-1995;
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                                                                                                                                                                                                                  AAR94477;
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Gaps
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increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal anti-inflammatory agents.

In a type (II or V) beta-turn specific human foetal artery smooth muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of 3.7 and 2.5, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      constrained backbone conformation; proinflammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated; mediated; increase; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C5a anaphylatoxin analogue C5a(65-74) Tyr65 Pro71 Ala72 D-Ala73.
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                                                                                                                                                                                                     Score 47; DB 17; Length 10;
Pred. No. 0.0034;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-terminal; human; C5a anaphylatoxin; analogue; beta-turn;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherman SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "D-form residue"
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Misc-difference 9
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                                                                                                                                                                                                                                                                                                                                                                                   AA.
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0
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                                                                                                                                                                                                        94.0%;
90.0%;
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                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                      1 YSFKDMPLXR 10
                                                                                                                                                                                                                                                                                       AA;
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                                                                                                                                                            Sequence
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                    (II or V) and type III beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (esp. vascular) permeability, respectively.
                                                                                              The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C5a anaphylatoxin C-terminal analogue C5a(65-74) Tyr65 Pro71 Ala72.
                                                                                                                                                                                              In a type (II or V) beta-turn specific human foetal artery smooth mascle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of 17.9 and 5.6, compared to 0.018 and 0.0013
backbone conformation (compared to the matural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal; human; C5a anaphylatoxin; analogue; beta-turn; constrained backbone conformation; proinflammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated; mediated; increase; cell membrane; vascular; permeability, neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; darug delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
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                                                                                                                                                                                                                                                                                                             88.0%; Score 44; DB 17; Length 10; 80.0%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                      2; Indels
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                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "beta-turn"
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                                                                                                                                                                                    anti-inflammatory agents.
                                                                                                                                                                                                                                                                                                                                      Conservative
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Matches 8; Conser
                                                                                                                                                                                                                                                                                                                                                                                     1 ysfkdmpaar 10
                                                                                                                                                                                                                                                                         10 AA;
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                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                      Matches
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region from human CSa anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible (c-terminal region) comprising a beta-turn. Analogues with type (II or V) and type III beta-turns elicit proinflammatory responses characterised by spasmogenesis, platclet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (esperascular) permeability, respectively.

The analogues can be used as immune adjuvants for the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In a type (II or V) beta-turn specific human foetal artery smooth muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of >1000 and 215, compared to 0.018 and 0.0013
                                                                      C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develophigh affinity C5a receptor antagonists useful as non-steroidal
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                                                                                                                                                                                                                                                                                                   The present peptide is an analogue of a C-terminal decapeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                            English.
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Best Local Similarity Bure.
The B; Conservative
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WPI; 1996-160140/16
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Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                 Kirnarsky L,
                                                                                                                                                                                                                                                                                      31-AUG-1994;
                                                             Homo sapiens
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                                                                                                Key
Region
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                                                                                                                                                                                                                                                                                                                                                                       The present peptide is an analogue of a C-terminal decapeptide region from human C5a anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with type C-terminal region) comprising a beta-turn. Analogues with type C-terminal region) compressly, platelet aggregation and neutrophil on mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil mediated increases in cell membrane (esp. creases and neutrophil mediated increases in cell membrane (esp. vascular) permeability, respectively. The analogues can be used as immune adjuvants for the treatment of timmune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by allocating and plate and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                              C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         In a type (II or'v) beta-turn specific human foetal artery smooth mustle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of 0.33 and 2.3, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders such as Alzheimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal anti-inflammatory agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune adjuvant; Immunodeficiency; augmentation; immune therapy;
cancer; drug delivery; CNS disorder; central nervous system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 17; Length 10; Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-terminal; human; C5a anaphylatoxin; analogue; beta-turn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                         Sherman SA, Taylor SM;
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                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 85; 116pp; English.
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80.0%;
                                                       95WO-US11126.
                                                                                                                                                                                       Sanderson DG,
                                                                                          94US-0299285
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Bost Local Similarity 80.0
Matches 8; Conservative
                                                                                                                              (UYNE-) UNIV NEBRASKA.
(UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                         WPI; 1996-160140/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 AA;
                                                                                                                                                                                       Kirnarsky L,
                                                     31-AUG-1995;
                                                                                          31-AUG-1994;
                                                                                                                                                                                                                                                                                                      permeability
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                 07-MAR-1996
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The present peptide is an analogue of a C-terminal decapeptide region from human C5a anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible (C-terminal region) comprising a beta-turn. Analogues with type (II or V) and type III beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (esp. vascular) permeability, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taylor SM;
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Pred. No. 0.034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sherman SA,
Location/Qualifiers
                                                                            /note= "beta-turn"
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1 ysfkdcplgr 10

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clior V) and type III beta-turns elicit proinfigamatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme reclease and neutrophil mediated increases in cell membrane (esp. vascular) permeability, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The analogues can be used as immune adjuvants for the treatment of immune deliciency disorders, and for augmenting standard immune thicknessy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affinity C5s receptor antagonists useful as non-steroidal anti-inflammatory agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal analogues of C5a anaphylatoxin · induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of 2.04 and 19.5, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present peptide is an analogue of a C-terminal decapeptide region from human C5a anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In a type (II or V) beta-turn specific human foetal artery smooth
                                                   C-terminal: human; C5a anaphylatoxin; analogue; beta-turn; constrained backbone conformation; proinflammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated; mediated; ccela membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
                  C5a anaphylatoxin analogue C5a(65-74) Tyr65 Cys70 Pro71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sherman SA, Taylor SM;
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               /note= "beta-turn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kirnarsky L, Sanderson DG,
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                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      WO9606629-A1
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Region
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response to an immunogen. The molecular adjuvant comprises a targeting response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting binding of the molecular adjuvant to the immunogen, and so binding of the molecular adjuvant to the APC determinant activates the APC, effecting delivery of the APC immunogen to an antigen presenting pathway of the APC. The present connected to an immune response for protecting adjuvant can be used to produce an immune response for protecting adjuvant can be used to pathogens or to produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiagnostic and immune agents. The molecular adjuvant is readily taken up and provide for the production of antibodies for use as immunodiagnostic and immune production of antibodies for use as immunodiagnostic and provide for the production of antibodies adjainst a weakly-antigenic or non-antigenic substances.
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                                                                                                                                                          Molecular adjuvant; immune response; immunogen; binding affinity; antigen presenting cell; APC; viral pathogen; anti tumour response; antibody; immunodiagnostic; immunotherapeutic; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular adjuvants for enhancing immune responses - comprise an immunogen linked to a ligand having binding affinity for a determinant of an antigen presenting cell
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Pred. No. 0.034;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hollingsworth MA, Sanderson SD, Tempero RA;
                                                                                                                                                                                                                                                                                                /note= "D-form residue"
                                                                                                                                  Molecular adjuvant targeting ligand.
                                                                                                                                                                                                                                                      Location/Qualifiers
9
                               AAW27250 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 51; 61pp; English.
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80.0%;
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                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYNE-) UNIV NEBRASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-244854/22.
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                    20-0CT-1995;
                                                                                                                                                                                                                                                                                                                                   W09714426-A1
                                                                                                 23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                    24-APR-1997
                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                AAW27250;
 11
             AAW27250
RESULT
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Gaps

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Score 42; DB 17; Length 10; Pred. No. 0.034; 0; Mismatches 2; Indels

84.0%; 80.0%;

Ouery Match Best Local Similarity 80.07

1 YSFKDMPLXR 10

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12

RESULT

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AAW27256
             RESULT
                                                          response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ligand being functionally linked to the immunogen, and so binding of the molecular adjuvant to the APC determinant activates the APC, effecting delivery of the immunogen to an antigen presenting pathway of the APC. The present sequence represents a specifically claimed formula for a molecular adjuvant, where the immunogen is serum amyloid A. The molecular and other pathogens or to produce an immune response for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapeutic agents. The molecular adjuvant is readily taken up and processed by APCs to provide APC-mediated immune responses. It can provide for the production of antibodies against a weakly-antigenic or
                                                                                                                                                                                              'note= "Serum amyloid A is attached to the N-terminal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A novel molecular adjuvant has been developed for enhancing an immune
                                                                                                    Molecular adjuvant; immune response; immunogen; binding affinity; antigen presenting cell; APC; viral pathogen; anti tumour response; antibody; immunodiagnostic; immunotherapeutic; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecular adjuvants for enhancing immune responses · comprise an immunogen linked to a ligand having binding affinity for a determinant of an antigen presenting cell
                                                                                                                                                                                                                                 /note= "Aminohexanoic acid which is a linear
                                                                                                                                                                                                                                              aliphatic spacer moiety"
                                                                                                                                                                                                                                                                                                                                                                                                               Tempero RA;
                                                                                                                                                                                                                                                                    /note= "D-form residue"
                                                                                                                                                                         Location/Qualifiers
         AAW27254 standard; peptide; 12 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 53; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Hollingsworth MA, Sanderson SD,
                                                                                                                                                                                                                                                                                                                                         96WO-US16825
                                                                                                                                                                                                                                                                                                                                                               95us-0005727
                                                                               Molecular adjuvant formula.
                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-244854/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
                                                                                                                                                                                                                                                         Misc-difference
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Modifled-site
                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                               20-OCT-1995;
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                                                      23-DEC-1997
                                                                                                                                                                                                                                                                                                                  24 - APR - 1997
                                                                                                                                                  Synthetic
                                AAW27254;
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AAW27254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     terminus. The molecular adjuvant can be used to produce an immune response for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiagnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and processed by APCs to provide APC-mediated immune responses. It can provide
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                                                                                                                                                                                                                                                                       Molecular adjuvant, immune response; immunogen; binding affinity, antigen presenting cell; APC; viral pathogen; anti tumour response; antibody; immunodiagnostic; immunotherapeutic; agonist.
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for a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 18; Length 18; Pred. No. 0.064; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular adjuvants for enhancing immune responses - immunogen linked to a ligand having binding affinity determinant of an antigen presenting cell
                                                                                                                                                                                                           Molecular adjuvant targeting ligand and immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tempero RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
AAW27256 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 31; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hollingsworth MA, Sanderson SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-US16825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-antigenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNE-) UNIV NEBRASKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-244854/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YSFKDMPLXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9714426-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-OCT-1996;
                                                                                                                                       23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                   AAW27256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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14

RESULT

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Gaps

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Score 42; DB 18; Length 12; Pred. No. 0.041; 0; Mismatches . 2; Indels

84.0%; 80.0%;

Query Match
Best Local Similarity 80.0
Matches 8; Conservative

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C5a anaphylatoxin analogue C5a(65-74) Tyr65 Gly69 Pro70.
                              17-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            response to an immunogen. The molecular adjuvant comprises a targeting response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen prosenting cell (APC), the targeting ligand being functionally linked to the immunogen, and so binding of the molecular adjuvant to the APC determinant activates the APC, effecting delivery of the immunogen to an antigen presenting pathway of the APC. The present sequence represents a specifically claimed targeting ligand and immunogen to molecular adjuvant can be used to produce an immune response for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiaynostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and processed to the production of antibodies against a weakly-antigenic or
                                                                                                                                                                                                                                                                               Molecular adjuvant; immune response; immunogen; binding affinity; antigen presenting cell; APC; viral pathogen; anti tumour response; antibody; immunodiagnostic; immunotherapeutic; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular adjuvants for enhancing immune responses - comprise an immunogen linked to a ligand having binding affinity for a determinant of an antigen presenting cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 19;
                                                                                                                                                                                                                          Molecular adjuvant targeting ligand and immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 18;
Pred. No. 0.068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tempero RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
18
                              AAW27251 standard; peptide; 19 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hollingsworth MA, Sanderson SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 52; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US16825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0005727
                                                                                                                                                             (first entry)
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-antigenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNE-) UNIV NEBRASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-244854/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9714426-A1
                                                                                                                                                          23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-1997
                                                                                          AAW27251;
                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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AAW27251
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   backbone conformation (compared to the natural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with Hype C-terminal region) comprising a beta-turn. Analogues with Hype (II or V) and type III beta-turns elicit prointlammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vascular) permeability respectively.
The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by disorders such as Alzheimer's disease or tumours, and to developing high affinity C5a receptor antagonists useful as non-steroidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-ferminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-inflammatory agents.
In a type (II or V) beta-turn specific human foetal artery smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of 0.59 and 2.0, compared to 0.018 and 0.0013
                                                                                                                                   mediated; increase; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present peptide is an analogue of a C-terminal decapeptide
                                                                               C-terminal; human; C5a anaphylatoxin; analogue; beta-turn; constrained backbone conformation; proinflammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region from human C5a anaphylatoxin, which has a constrained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 17; Length 10;
Pred. No. 0.054;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Taylor SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherman SA,
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    /note= "beta-turn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 87; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                95WO-US11126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanderson DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94US-0299285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYNE-) UNIV NEBRASKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-160140/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kirnarsky L,
                                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-AUG-1994;
                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         W09606629-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    permeability
                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-1996
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                                                                                                                                                                                                                                                                                                                       Region
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Gaps

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2; Indels

0; Mismatches

ò S AAR94486 standard; peptide; 10 AA.

RESULT 15 AAR94486 AAR94486;

2 × 2

1 YSFKDMPLXR 10 |||| ||| || | | ysfkgmplyr 10

o o

Search completed: February 27, 2002, 11:41:13 Job time: 452 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein – protein search, using sw model

February 27, 2002, 11:45:12 ; Search time 145.23 Seconds
(without alignments)
5.245 Million cell updates/sec Run on:

US-09-446-109A-3 Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 YSFKDMPLXR 10 Scoring table: Sequence:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	nydroxymetnylbilan	S	probable tail-host	probable tail-host	type II site-speci	hypothetical prote	fibronectin-bindin	probable mitochond	hydroxymethylbilan	threoninetRNA li	collagen adhesin -	hypothetical prote	conserved hypothet	hypothetical prote	restriction endonu	probable ubiquinon	gene 8 protein - p		hypothetical prote	transcription fact.	Ets-related transc	cytochrome-c oxida	probable DNA helic	ATP-dependent heli	hypothetical prote	cyritestin precurs	cation efflux syst	protein F2 - Strep	hypothetical prote
	ID	140810	G02318	T09204	T09273	A81166	C71414	533851	562485	A69405	YSBST2	A42404	T19459	F83085	T24789	S71507	T41372	S58138	850590	T21510	JC7576	A43361	E69609	D71493	C81652	T01539	S18968	F70342	T30856	T49500
	DB	 7	~	~	~	7	~	~	7	7	-	7	7	7	7	~	7	7	7	7	m	7	7	~	~	7	~	7	7	7
	Length	295	581	1276	1291	489	555	1117	271	289	638	1185	1469	1516	230	260	305	382	576	593	615	619		634		773	823	1019	1039	1421
æ	Query Match	72.0	72.0	72.0	~	70.0	0.89	0.89	9.9	0.99	99	99	0.99	99	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0	64.0		64.0	64.0	64.0	64.0	64.0	. 64.0
	Score	36	36	36	36	35	34	34	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
	Result No.	-	7	m	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 11-6c-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
Ciscession: G02318
Ribbermann, T.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01044
A:Reference number: H01044
A:Reference rumber: H01044
A:Recession: G02318
A:Accession: G02318
A:Accession: G02318
A:Residues: 1-581 < LIB>
A:Residues: 1-581 < LIB>
A:Residues: 1-581 < LIB>
Ciscentics: 1-581 < LIB

A.Gena: NERF-2 C.Superfamily: ets PMA-binding domain homology F;198-278/Domain: ets DNA-binding domain homology <FTS>

conserved hypothet	genome polyprotein	probable cell-surf	H+-transporting AT	phosphoinositide 3	phosphoinositide 3	conserved hypothet	hypothetical prote	structural protein	hypothetical prote	hypothetical prote	conserved hypothet	pyruvate dehydroge	hypothetical prote	translation initia	middle Tantigen -
S20614	JQ1657	S27852	T44673	PC4346	PC4345	D69887	A64029	T12734	D81315	F71851	E69195	A71681	T20266	A81464	TVVPM
7	-	7	7	7	7	7	7	7	7	7	7	~	7	~	ri
1738	1864	3229	102	131	131	170	201	243	265	285	317	326	378	403	440
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64	64	64	62	62	62	62	62	62	62	62	62	6.5	62	62	62
32	32	32	31	31	31	31	31	31	31	31	3.1	31	31	31	31
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

ALIGNMENTS

	RESULT 1 140810
	hydroxymethylbilane synthase (EC 4.3.1.8) - Clostridium josui N;Alternate names: porphobilinogen deaminase
	C;Species: Clostridium josui C;Date: 16-Auq-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
_	C;Accession: 140810
_	R.F.Ujino, E.; Fujino, T.; Ratita, S.; Sakka, K.; Ohmiya, K.
	J. Bacteriol. 177, 2169-2173, 1993 A;Title: Cloning and sequencing of some genes responsible for porphyrin biosynthesis
	A:Reference humber: A57344; MUID:95394829
	A; Accession: I40810
	A;Status: preliminary; translated from GB/EMBL/DDBJ
_	A; Molecule type: DNA
	A:Residues: 1-295 <res></res>
	A;Cross-references: GB:D28503; NID:9536874; PIDN:BAA05861.1; PID:9460692
	C; Genetics:
_	A;Gene: hemC
_	C;Superfamily: hydroxymethylbilane synthase
_	C; Keywords: ammonia-lyase; carbon-nitrogen lyase; porphyrin biosynthesis
	F;237/Modified site: dipyrrolylmethanemethyl (Cys) (covalent) #status predicted
_	Query Match 72.0%; Score 36; DB 2; Length 295;
	sal Similarity 75.0%;
	o; caps
	Qy 1 YSFKDMPL 8
_	DD 82 HSYKDMPC 89
_	

2

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C, Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 2
Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                            70.08;
75.08;
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85.7%;
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0v
That 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 4COP9-4G3845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
..... 6; Conserv?
                                                                                                                A;Residues: 1-489 <TET>
A;Cross-references: GB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 :111
267 YSFSEMPL 274
                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YSFKDMPL 8
                                                                                           A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: C71414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YSFKDMP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A: Variety: columbia
                                                                                                                                                                                   C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S33851
                                                                                                                                                                                                                                                                                                                                                                                                                       ογ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable tall-host specificity protein - Streptococcus thermophilus phage Sfil9 C:Species: Streptococcus thermophilus phage Sfil9 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000 C:Accession: T09273 Fsequence_revision 20-Sep-1999 #text_change 11-May-2000 C:Accession: T09273 Fsequence_revision 4. Brussow, H. Virology 241, 345-356, 1998 Fsequence revision of Streptococcus thermophilus bacteriophage genomes by modular exchan A:Reference number: 216607; MUID:98160788
                                                                                                                                                                                                                                               probable tail-host specificity protein - Streptococcus thermophilus phage Sfi21
C; Species: Streptococcus thermophilus phage Sfi21
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C; Accession: T. Lucchini, S.; Brussow, H.
Virology 241, 345-356, 1998
A:Title: Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchart A:Reference number: 216607; MUID:98160788
A:Reference number: 216607; MUID:98160788
A:Status: translated from GB/EMBL/DDBJ
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R:Tettelin, H.: Saunders, N.J.: Heidelberg, J.: Jeffrics, A.C.: Nelson, K.E.: Eisen, J.A. Hickoy. E.K.: Haft, D.H.: Salzberg, S.L.: White, O.: Fleischmann, R.D.: Dougherty, B.A.: Ti, H.: Oin, H.: Vamalhevan, J.: Gill, J.: Scarlato, V.: Masignani, V.: Pizza, M. Science 287, 1809-1815, 2000
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Pred. No. 36;
1; Mismatches 1; Indels
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Score 36; DB 2; Length 581;
Pred. No. 15;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residuca: 1-1276 cDLS>
A:Cross-references: EMBL:AF032121; NID:g2935667; PID:g2935676
C;Keywords: tall protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL: AF032122; NID: 92935682; PID: 92935691
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75.0%;
72.0%;
85.7%;
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Best Local Similarity 75.v.
6; Conservative
72.0
Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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A; Residues: 1-1291 <DES>
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259 YSFKDSPM 266
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259 YSFKDSPM 266
                                                                                                                   1 YSFKDMPL 8
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AB1166
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RiBevan, M.: Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D. P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; G. avanagh, T.; Hempel, S.; Kotter, P.; Entlan, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Axauthors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomen erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.;
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                                                                                                                                                                                                                                                                                                                                    A:Gene: NWB0726
C;Superfamily: Haemophilus paragallinarum type II site-specific deoxyribonuclease Hga
C;Keywords: hydrolase
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C:Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 15-Oct-1999
C:Accession: S33851; S3261; S32651
C:Accession: S33851; S32631, M.J.; Signaes, C.; Guss, B.; Gurusiddappa, S.; Hoeoek, M.; Eur. J. Biochem. 214, 819-827, 1993
A:Title: Two different genes coding for fibronectin-binding proteins from Streptococc A; Reference number: S33850; MUID:93307299
                                                                                                                                                                                                                          A;Cross-references: GB:AE002428; GB:AE002098; NID:g7225959; PIDN:AAF41139.1; PID:g722
A;Experimental source: serogroup B, strain MC58
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755
A;Accession: A81166
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A;Residues: 1-1117 <LIN>
A;Cross-references: EMBL:222151; NID:9288970; PIDN:CAA80122.1; PID:9581643
A;Note: the authors translated the initiation codon TTG for residue 1 as Leu
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998
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Pred. No. 20;
1; Mismatches
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, Am.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Febret, C.; Ferrari, Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujila, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsapel, S.; Hosono, S.; Hillo, M.; Koetter, P.; Koningstein, G.; Krogh, S.; Kurina, M.; Kurina, K.; Lapidus, A.; Lardin, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau, Y.; M.; Ogawa, K.; Ogiwara, A.; Ogiwara, A.; Ogiwara, A.; Ogiwara, A.; Ogiwara, A.; Ogiwara, A.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sato, T.; Scanl A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sato, T.; Scanl A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Ochiya A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tata, K.; Yoshida A; Authors: Complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A6580; MUID:98044033
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C:Species: Staphylococcus aureus
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 10-Nov-1995
C:Accession: A42404; $27665
R:Patti, J.M.: Jonsson, H.: Guss, B.: Switalski, L.M.: Wiberg, K.: Lindberg, M.: Hook
J. Biol. Chem. 267, 4766-4772, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Putzer, H.; Brakhage, A.A.; Grunberg-Manago, M.
J. Bacteriol, 172, 4953-4602, 1990
A;Title: Independent genes for two threonyl-tRNA synthetases in Bacillus subtilis.
A;Reference number: A37770; MUID:90330571
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C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 16-Jun-2000
C:Accession: A37770; C69723
                                                                                                                                                                                                                                                                                                                                                                                                                                        threonine--tRNA ligase (EC 6.1.1.3) thrz [validated] - Bacillus subtilis N:Alternate names: threonine--tRNA ligase, minor; threonyl-tRNA synthetase
                                                                                          Gaps
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C;Superfamily: threonine--LRNA ligase
C;Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
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        Length 289;
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    ore 33; DB;
ed. No. 30;
Mismatches
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        Score 33;
Pred. No.
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                                                                                      Conservative
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    Query Match
Best Local Similarity
Matches 6; Couserv
                                                                                                                                                            1 YSFKDMPLXR 10
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A: Residues: 1-638 <PUT>
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Best Local Similarity
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348 YSYRDLPI 355
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Nydroxymethylbilane synthase (EC 4.3.1.8) - Archaeoglobus fulgidus
C.Space.
C.Sp
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A:Cross-references: GB:AE001018; GB:AE000782; NID:g2689341; PIDN:AAB90000.1; PID:g264933 C:Superfamily: hydroxymethylbilane synthase C:Superfamily: hydroxymethylbilane synthase C:Keywords: ammonia lyase; carbon-nitrogen lyase; porphyrin biosynthesis F:234/Modified site: dipyrrolylmethanemethyl (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-raferences: EMBL:256276; NID:91022345; PIDN:CAA91209.1; PID:91022353; GSPDB:GNOC
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C:Superfamily: ADP.ATP carrier protein repeat homology
F:1-75/Domain: ADP.ATP carrier protein repeat homology #status atypical <ACPl>
F:80-164/Domain: ADP.ATP carrier protein repeat homology <ACP2>
F:170-269/Domain: ADP.ATP carrier protein repeat homology <ACP3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable mitochondrial carrier - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Species: 16-May 131896 sequence_revision 13-Mar-1997 #text_change 10-Dec-1999 C;Accession: T38853; S62485 R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, October 1995 A;Reference number: 221745 A;Reference number: 221745
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                        A.Start codon: TTG C.Keywords: fibronectin binding C:Keywords: fibronectin binding F:1-21/Domain: signal sequence *status predicted <SIG> F:21-21/Domain: signal sequence *status predicted <MAT> F:28-1117/Product: fibronectin-binding protein *status predicted <MAT>
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Pred. No. 28;
1; Mismatches
                                                                                                                                                                                                                                                               Score 34; DB 2;
Pred. No. 81;
2; Mismatches
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75.0%;
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-271 <BA2>
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531 YTFKDLP 537
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A:Gene: fnbB
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A; Molecule type: DNA
A; Residues: 1-260 CUEN>
A; Residues: 1-260 CUEN>
A; Cross-references: EMBL:DB2028; NID:g1620875; PIDN:BAA11515.1; PID:g1620877
A; Experimental source: ATCC 15831
A; Note: the amino end of this sequence was confirmed by protein sequencing
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1996
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1996
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C.Superfamily: Brevibacterium albidum restriction endonuclease Ball
C.Keywords: endonuclease; hydrolase; methyltransferase; restriction modification syst
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restriction endonuclease (EC 3.1.-.-) Ball - Brevibacterium albidum (ATCC 15831)
C.Species: Brevibacterium albidum
A:Variety: ATCC 15831
C.Date: 29-Jan-19-9 #sequence_revision 1.3-Feb-1998 #text_change 20-Jun-2000
C.Accession: S71507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Cross-references: EMBL:293388; PIDN:CAB07655.1; GSPDB:GN00023; CESP:T10C6.5
A:Experimental source: clone T10C6
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Aritte: Cloning and expression of the Ball restriction-modification system. A:Reference number: S71506: MUID:96279725
A;Reference number: S71507
                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T10C6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequencc_revision 15-Oct.1999 #text_change 15-Oct-1999
C;Accession: T24789
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              Pred. No. 1.8e+02;
1; Mismatches 3;
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A:Molecule type: DNA
A:Residues: 1-230 <WIL>
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Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, March 1997 A;Reference number: 219936 A;Accession: T24789
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Best Local Similarity 62.5%;
Matches 5; Conservative
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85.7%;
              Best Local Similarity 60.0%;
Matches 6; Conservative
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Best Local Similarity 85.7
Matches 6; Conservative
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3 YAFRDRPL 10
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30 YSSKDMP 36
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A; Introns: 57/3
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Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A; Reference number: A82950; MUID:20437337
A; Reference number: A82950; MUID:20437337
A; Residues: I-1516 cS7D>
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A:Introns: 119/1; 232/2: 315/3; 369/3; 464/2; 535/2; 612/1; 864/3; 965/3; 1038/3; 1113/
A;Title: Molecular characterization and expression of a gene encoding a Staphylococcus A;Reference number: A42404; MUID:92165839
A;Contents: FDB 574
A;Contents: FDB 574
A;Accession: A42404
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1185 < PAT>
A;Coss-references: EMBL:N81736
A;Note: sequence extracted from NCBI backbone (NCBIP:83982)
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C; Species: deanorhabditis elegans
C; Species: deanorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C; Accession: T19459
R; Mortimore, B.
Submitted to the EMBL Data Library, November 1996
A; Reference number: 219126
A; Reference number: 219126
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1469 < WIL>
A; Residues: 1-1469 < WIL>
A; CESP: C25F9.2
C; Genetics: Clone C25F9
C; Genetics:
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Pred. No. 1.4e+02;
1; Mismatches 1; Indels
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ilarity 71.4%;
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Matches 5; Conserv
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583 YEFKDLP 589
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649 YSYKDVP 655
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methanococc
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caenorhabdi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q59293 clostridium
                                                                                                            February 27, 2002, 11:42:39 ; Search time 78.39 Seconds
(without alignments)
4.677 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        065361 q
019272 c
P08566 s
000750 h
P45154 h
Q445154 h
Q55360 u
P55360 u
P55360 u
P55360 u
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P48906
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               100059 seqs, 36664827 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEM3_CLOJO
YAD8_SCHPO
HEM3_ARCFU
RF3_STAAU
SYT2_BACSU
CNA_STAAU
MAUJ_METEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYB_CENSE
YAM_RHISN
UPP_PYRAB
Y009_METJA
GALR_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARO1_YEAST
PK3B_HUMAN
YFAE_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYPC_YEAST
ELET_MOUSE
ELET_HUMAN
COXI_BACSU
YCTE_EPTVI
VGNB_ECAV
VATF_DESSY
VATF_DESSY
YE1B_HAEIN
ODPA_RICPR
TRUB_THEAC
TRUB_THEAC
TRUB_THEAC
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MSH5_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Listing first 45 summaries
                                                                          - protein search, using sw model
                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                   US-09-446-109A-3
                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                 1 YSFKDMPLXR 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
                                                                                                                                                                                             Title:
Perfect score:
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                                                                              OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                  Run on:
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044960 caenorhabdi 099v76 deinococcus P10507 saccharomyc 009736 schizosacch 079672 pelomedusa P47615 mycoplasma P47615 mycoplasma P47615 solamum tub 090775 solamum tub 092mv3 helicobacte P56071 helicobacte 091819 drosophila	ALIGNMENTS BESULT 1 10.10.00 BHIST.CLOJO BHIST.CLOJO BHIST.CLOJO BHIST.CLOJO BHIST.CLOJO BHIST.CLOJO BHIST.CLOJO STANDARD; BFT; 295 AA. 10.10.WO-1997 (Rel. 35, Created) 10.10.WO-1997 (Rel. 35, Last sequence update) 10.10.WO-1997 (Rel. 36, Last amnotation update) 10.10.WO-1997 (Rel. 10.10.Wo-19) 10.10.Wo-1997 (Rel. 10.10	EAEGO CRC64;
NH64_CAEEL ALN_DEERA MPRP_YEAST CP51_SCHPO COV1_PELSU SYT_MYCGE MRHL_WOLSU VGST_SOLTU SYT_HELPJ SYT_HELPY CONN_DROME IF2M_SCHPO	ALIGNMENTS T. 1 T. 292 AA. T. 29293 T. 201-NOV-1997 (Rel. 35, Last sequence update) T. 20-AUG-2001 (Rel. 40, Last annotation update) T. 20-AUG-2001 (Rel. 36, Last sequence update) T. 20-AUG-2001 (Rel. 36, Last sequence update) T. 20-AUG-2001 (Rel. 36)	MW; C0037415E92EAE60 CRC64;
60.0 4412 1 60.0 60.0 4418 1 60.0 60.0 4418 1 60.0 60.0 554 1 60.0 60.0 60.0 60.0 60.0 60.0 60.0 60	11.00JO STANDARD: 30293; 31.00V-1997 (Rel. 35, Last 20.00V-1997 (Rel. 35, Last 20.00V-1997 (Rel. 35, Last 20.00FPHOBILINOGEN DEAMIANASE SYNTHASE) (HMBS) (PRE-UNCOP- HMBS) (HMBS) (PRE-UNCOP- LIOSTRIALM DASHI SACCERTIAL TAID—149; [1] SACCERTIAL TAID—149; [1] STRAIN—EERM P-9684; MEDLINE—95394829; PubMed—7 MEDLINE—95394829; PORPHDDMI MEDLINES REQUISE BIOST 1	32744 32744
	T 1 CLOJO HEM3_CLOJO ST. 01-NOV-1997 (Rel. 01-NOV-1997 (Rel. 01-NOV-1997 (Rel. 01-NOV-1997 (Rel. 020-AUG-2001 (Rel. 020-AUG-2001 (Rel. 020-AUG-2001 (Rel. 020-AUG-2001 (Rel. 020-AUG-2001 (Rel. 020-AUG-2001 (Rel. 030-AUG-2001 (Rel. 030-AUG-200	SEQUENCE 29
W W W W W W A A A A A A A A A A A A A A	RESULT HEM3_CLOJO DT HEM3_CLOJO DT O1-NO DE SYNTH GN HEMC. OC CLOST OC CLOST CC CLOST CC CC CC TT CLOST CC	

Gaps

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72.0%; Score 36; DB 1; Length 295; 75.0%; Pred. No. 3; tive 2; Mismatches 0; Indels

Query Match 72.0 Best Local Similarity 75.0 Matches 6; Conservative

1 YSFKDMPL 8

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Ludovice A.M., Wu S., de Lencastre H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1280
                                                                                                                                                                                           Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRFC OR RF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RF3_STAAU
086490;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RF3_STAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
PROBABLE PORPHOBILINGEN DEMINASE (EC 4.3.1.8) (PBG)
(HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINGEN SYNTHASE).
                                                                                                                                                                                                                                                                                         STRAIN*972;
Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (POTENTIAL).
-!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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0
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Pfam: PF00153; mitocarr; 3.
PROSITE: PS00215; MITOCH_CARRIER; 1.
Hypothetical protein: Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilEMC OR AF1242.
Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
EF330C8CC8BDB6C4 CRC64;
                                                                                                         Ol-FEB-1996 (Rel. 33, Created)
Ol-FEB-1996 (Rel. 33, Last sequence update)
Ol-FEB-1996 (Rel. 33, Last annotation update)
Ol-FEB-1996 (Rel. 33, Last annotation update)
PUTATIVE MITOCHONDRIAL CARRIER C4GB.08
SPAC4GB.08
Schlzosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl; Ascomycota; Schlzosaccharomycetes; Schlzosaccharomycetaes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30002 MW;
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                                                                                   STANDARD;
                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
          82 HSYKDMPL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :111 111
36 FSFKTMPL 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-2234;
                                                                                                                                                                                                                                                 NCBI_TaxID-4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YSFKDMPL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaeoglobus
                                                                                 YAD8_SCHPO
Q09834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEM3_ARCFU
029026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
HEM3_ARCFU
ID HEM3_A
AC 029026
DT 30-MAY
DT 30-MAY
DT 20-VI
DE PROBNB
DE (HYDRO
CON HIEMC OO
CON ARCHAGE
OC ARCHAGE
                                                                    YAD8_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY).

*!- CATALYTIC ACTIVITY: 4 PORPHOBILINOGEN + H(2)0 =
HYDROXYMETHYLBILIANE + 4 NH(3).

-!- COFACTOR: COVALENTLY BINDS A DIPYRHOMETHANE COFACTOR TO WHICH
THE PORPHOBILINOGEN SUBBUNTS ARE ADDED (BY SIMILARITY).

-!- PATHWAY: FOURTH STEP IN PORPHYRIN BIOSYNTHESIS BY THE C5 PATHWAY.

-!- SIMILARITY: BELONGS TO THE HMBS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: TETRAPOLYMERIZATION OF THE MONOPYRROLE PBG INTO THE HYDROXYMETHYLBILANE PREUROPORPHYRINGGEN IN SEVERAL DISCRETE STEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
PETRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
Klenk H.-P., Clayton R.A., Todson R.J., Carina J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.L., McNeil L.K., Badger J.H., Glodek A., Zhou L.
Overbeek R., Gocayne J.D., Weidman J.F., McNonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porphyrin biosynthesis; Lyase; Complete proteome.
BINDING 234 234 PYRROMETHANE COFACTOR (BY SIMILARITY).
SEQUENCE 289 AA; 32006 MW; E3527A0F9C09C78C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01379; Porphobil_deam; 1.
PRINTS; PR00151; PORPHBDMNASE.
PROSITE; PS00533; PORPHOBILINOGEN_DEAM; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PEPTIDE CHAIN RELEASE FACTOR 3 (KF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.0%; Score 33; DB
60.0%; Pred. No. 13;
Live 2; Mism...ches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000860; Porphobil_deam.
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CNA_STAAU
Q53654;
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                                               EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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CNA_STAAU
CNA_STAAU
AC 05365
AC 05365
DT 15-DEB
DT 15-DEB
DT 15-DEB
DT 15-DEB
COLLA
COC Bacite
OC Bacite
OC Bacite
COC Bact
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                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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*Molecular cloning and DNA sequencing of the Staphylococcus aureus UDP-N-acetylmuramyl tripeptide synthetase (murE) gene, essential for the optimal expression of methicillin resistance."; Microb. Drug Resist. 4:85-90(1998).

-!- FUNCTION: INCREASES THE FORMATION OF RIBOSOMAL TERMINATION COMPLEXES AND STIMULATES ACTIVITIES OF RF-1 AND RF-2. IT BINDS GUANINE NUCLEOTIDES AND HAS STRONG PREFERENCE FOR UGA STOP CODONS. IT MAY INTERACT DIRECTLY WITH THE RIBOSOME. THE STIMULATION OF RP-1 AND RF-2 IS SIGNIFICANTLY REDUCED BY GTP AND GDP, BUT NOT BY
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                                                                                                                                                                                                GMP (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Putzer H., Gendron N., Grunberg-Manayo M.; "Co-ordinate expression of the two threonyl-tRNA synthetase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
THREONYL-TRNA SYNTHETASE 2 (EC 6.1.1.3) (THREONINE--TRNA LIGASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Putzer H., Brakhage A., Grunberg-Manago M.;
"Independent genes for two threonyl-tRNA synthetases in Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glaser P., Sekowska A., Danchin A.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTP (BY SIMILARITY).
C39D8DB5F4BBE460 CRC64;
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Bacillus/Staphylococcus group: Bacillus.
NCBL_TaxID-1423;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000795; GTP_EFTU.
Pagn; PF00009; GTP_EFTU.
PROSITE: PS00301; EFACTOR_GTP; FALSE_NEG.
Protein blosynthesis; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=90330571; Pubmed=2115870;
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 521 AA;
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Bacillus subtilis.
                                                                                                                                                                                                                                                                       PRFC SUBFAMILY
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380 YSFQDLP 386
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P18256; P70992;
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SEQUENCE
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Prof. 
                                                                                                                                                                                                                                                                                                                                                                                               -i. DEVELOPMENTAL STAGE: NORMALLY NOT EXPRESSED. ITS EXPRESSION IS INDUCED WHEN THAT OF THRS IS REDUCED.
-i. SIMILARITY: BELONGS TO CLASS-II AMINOACYL.TRNA SYNTHETASE FAMILY.
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Staphylococcis areas collagen adhesin.";
J. Biol. Chem. 557:4766-4772(1992).
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ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
V -> L (IN REF. 2).
D61922564598975A CRC64:
Bacillus subtilis: control by transcriptional antitermination
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Lindberg M., Hornek M.;
                                                                                                                                   -:- CATALYTIC ACTIVITY: ATP + L-THREONINE + TRNA(THR) = AMP PYROPHOSPHATE + L-THREONYL-TRNA(THR).
-:- COFACTOR: BINDS ONE ZIVO ION (BY SIMILARITY).
-:- SUBGNUT: HOMODIMER (BY SIMILARITY).
-:- SUBGELLULAR LOCATION: CYTOPLASMIC.
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29;
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NCBI_TaxID=1280;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                    nvolving a conserved regulatory sequence."; SMBO J. 11:3117-3127(1992).
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EMBL: 280360; CAB07510.1; -.
EMBL: 299123; CAB15783.1; -.
FIR: A37770; YSBST2.
Subtilist; BG10421; thrz.
InterPro: IPR002106; AALENA_ligase_II.
InterPro: IPR002314; tRNA_synt_2b.
InterPro: IPR002314; TRNA_synt_thr.
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MEDLINE-92165839; PubMed=1311320;
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50.0%;
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387
512
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Best Local Similarity
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Usage by and for commercial
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01-FEB-1995 (Rel. 31, Last sequence update)
01-ROV-1997 (Rel. 35, Last annotation update)
PROBABLE PROLYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.15) (PROLINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYROPHOSPHATE + L-PROLYL-TRNA(PRO).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
-!- SIMILARITY: BELONGS TO CLASS-II AMINVACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                       Chistoserdov A.Y., Chistoserdova L.V., McIntire W.S., Lidstrom M.E., "Genetic organization of the mau gene cluster in Methylobacterium extoquens AMI: complete nucleotide sequence and generation and characteristics of mau mutants."; J. Bacteriol. 176:4052-4065(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERMINESTRY NOT ALL AND STATE OF THE PROBLEM OF TRANSPACE OF THE PROBLEM OF TRANSPACE OF THE PROBLEM OF THE OF
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Eukaryota; Fungi; Ascomycota; Saccharomycolina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32; DB 1; Length 295;
Pred. No. 21;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L26406; AAB46938.1; -.
SEOUENCE 295 AA; 32682 MW; 7FE490E025D99191 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                              Methylobacterium group; Methylobacterium.
METHYLAMINE UTILIZATION PROTEIN MAUJ.
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-AM1 / NCIB 9133;
MEDLINE-94292425; Pubmed-8021187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.0%;
85.7%;
                                                                     Methylobacterium extorquens
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Best Local Similarity 85.77
در 6: Conservative
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                                                                                                                                                                                     NCBI_TaxID=408;
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P39965;
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CONSERVED IN GRAM-POSITIVE COCCI SURFACE
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                                                                                                                                                                                                                                                                                                                            Patti J.M., Boles J.O., Hoeoek M.;
"Identification-and biochemical characterization of the ligand
binding:domain of the collagen adhesin from Staphylococcus aureus.";
Biochemistry 32:11428-11435(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Struct. Biol. 4:833-838(1997).

FUNCTION: MEDIATES ATTACHMENT OF STAPHYOCOCCAL CELLS TO COLLAGEN-CONTRINING SUBSTRATA.

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. CELL WALL.

SINILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 169-318.
MEDLINE-97475225; Pubmed-9334749;
Symersky J., Pattl J.M., Carson M., House-Pompeo K., Teale M.,
MOORE D., Jin L., Schneider A., DeLucas L.J., Hoeoek M.,
Narayana S.V.L.;
"Structure of the collagen-binding domain from a Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
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                                                                         Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
MEMBRANE ANCHOR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
COLLAGEN-BINDING.
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InterPro; IPRO01899; Gram_pos_anchor.
PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
PROSITE: Repeat; Transmembrane; Cell wall; 3D-structure.
POTENTIAL.
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(Rel. 35, Last sequence update)
(Rel. 35, Last annotation update)
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1; Mismatches
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                                                                                                Lindberg M., Hoeoek M.;
J. Biol. Chem. 269:11672-11672(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 x 187
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MEDLINE-94032261; Pubmed-8218209;
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Best Local Similarity 71.4%,
Las 5; Conservative
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                                                                                                                                                                                                                    COLLAGEN-BINDING DOMAIN.
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01-NOV-1997
01-NOV-1997
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Q49127;
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PIR; A43361; A43361
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SEQUENCE
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 DR KW TF SO
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XX MEDLINE=9657231; Pubmed=8666284;

XX MEDLINE=9657231; Pubmed=8666284;

XX Davis J.N. Roussel M.F.;

**Cloning and expression of the murine Elf-1 cDNA.";

Gene 171:265-269(1996);

IL Gene 171:265-269(1996);

Y-CELL-RECEPTOR-MEDIATED TRANS ACTIVATION OF HIV-2 GENE

EXPRESSION. BINDS SPECIFICALLY TO TWO PURINE-RICH MOTTES IN THE

HIV-2 ENHANCERE. ELF-1 BINDS TO THE UNDERPHOSPHORYLATED FORM OF RB.

MAY INTERACT WITH OTHER TRANSCRIPTION FACTORS IN ORDER TO REGULATE

SPECIFIC GENES (BY SIMILARITY).

1. SUBCELLULAR LOCATION: NUCLEAR.

2. TISSUE SPECIFIC GELLS.

DETECTED IN OTHER CELL TYPES SUCH AS FIBROBLASTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                           InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002314; tRNA-synt_2b.
InterPro; IPR002316; tRNA-synt_bro.
InterPro; IPR002316; tRNA-synt_bro.
PR015; PR001046; TRNASYNTHPRO.
PR05TTE; PS00179; AA_TRNA_LIGASE_II_1; 1.
PR05TTE; PS00179; AA_TRNA_LIGASE_II_2; FALSE_NEG.
AA_NINOACY!TRNA synthetase; Protein blosynthesis; Ligase; ATP-binding.
SEQUENCE 576 AA; 65880 WW; D8C5BD76847CCAF3 CRC64;
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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0
                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ETS-RELATED TRANSCRIPTION FACTOR ELF-1 (E74-LIKE FACTOR 1).
                                                                                                                                                                                                  Score 32; DB 1; Length 576;
Pred. No. 43;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                         612 AA
                                                                                                                                                                                                                                                                                                                                          PRT;
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Interpro; IPR002341; HSF_ETS
                                                                                                                                                                                                    64.0%;
71.4%;
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                                     EMBL; U18839; AAB64642.1; -.
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PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                  SGD; S0000889; YER087W
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| 130 SYKDMPI 136
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Q60775;
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MEDILINE-92186836: PubMed=154787;
Thompson C. B., Mang C.Y., HO I.C., Bohjanen P.R., Petryniak B.,
June C.H., Miesfeldt S., Zhang L., Nabel G.J., Karpinski B.;
"Cis-acting sequences required for inducible interleukin-2 enhancer
function bind a novel Ess-related protein, Elf-1.";
Moi. Cell. Biol. 12:1043-1053(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A novel Ets-related transcription factor, Elf-1, binds to human immunodeficiency virus Lype 2 regulatory elements that are required for inducible trans activation in T cells."; J. Virol. 66:5890-5897(1992).
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
Nuclear protein; Transcription regulation; Activator; DNA-binding.
DOMAIN 75 80 POLY-ASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leiden J.M., Wang C.Y., Petryniak B., Markovitz D.M., Nabel G.J.,
Thompson C.B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P32519; OGUDE1;
01-ocT-1993 (Rel. 27, Created)
10-ocT-1993 (Rel. 27, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ETS-RELATED TRANSCRIPTION FACTOR ELF-1 (E74-LIKE FACTOR 1).
                                                                                                                                                                                                     Score 32; DB 1; Length 612;
Pred. No. 46;
                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                      ETS-DOMAIN.
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                                                                                                                                 66221 MW;
                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                      290
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                                                                                                                              612 AA;
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287 YQFKEMP 293
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announcc/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Heme; Copper; Transmembrane; Respiratory chain;
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47;
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COPPER B (PROBABLE).
IRON (HEME A3) (PROBABLE).
IRON (HEME A) (PROBABLE).
H -> G [IN REF. 1).
MISSING (IN REF. 1).
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EXTRACELLULAR (POTENTIAL).
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80159F21D1913068 CRC64;
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Pred. No. 47;
2; Mismatches
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EMBL; Z98682; CAB11343.1; -.
EMBL; Z99111; CAB13363.1; -.
PTR; S14397; S14397.
HSSP; P98002; 1AR1.
Subtilist: BG10216; ctab.
InterPro; IPR000883; COXI.
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                         PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50064; ETS_DOMAIN_3; 1.
Nuclear protein Transcription regulation; Activator; DNA-binding.
DOMAIN :: : : 75 8 POIN-ASP.
DNA_BIND: 208 290 ETS-DOMAIN.
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PATHWAY: TERMINAL STEP IN THE RESPIRATORY CHAIN.
SURCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS 14
POTENTIAL TRANSMEMBRANE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COXI_BACSU STANDARD: PRT; 622 AA. P24010: 034467: 01-MAR-1992 (Rel. 21, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1) (CYTOCHROME AA3 SUBUNIT 1) (CAA-3605 SUBUNIT 1).
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"The Bacillus subtilis cytochrome-c oxidase. Variations on a conserved protein theme.";
Eur. J. Blochem. 195:517-525(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32; DB 1; Length 619;
Pred. No. 46;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suraste M., Metso T., Nakari T., Jalli T., Lauraeus M.,
                                                                                                                                                                                                                                                                                                                                                    Q -> G (IN REF. 2).
AB0B41B2964A66EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. NCBL_Tax(D=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91146590; PubMed=1847686;
                                                                                                                                                                                                                                                                                                                                                 283 C
67455 MW;
                                                             InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.0%;
71.4%;
                                                                                                                   Pram; PF00178; Ets; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
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Best Local Similarity
5, Conservē
                    TRANSFAC; T01113; ..
                                                                                                                                                                                                                                                                                                                                                 283 ;
619 AA;
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287 YOFKEMP 293
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VATF_DESSY
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01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GENOME POLYPROTEIN B (CONTAINS: PROTENSE COFACTOR; MEMBRANE BINDING PROTEIN; VPG; PROTEASE (EC 3.4.22.-); RNA POLYMERASE (EC 2.7.7.48)].
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-92114084: Pubmed-1731088:
Wolfe K.H., worden C.W., Palmer J.D.;
"Small single-copy region of plastid DNA in the non-photosynthetic anglosperm Epifagus virginiana contains only two genes. Differences among dicots, monocots and bryophytes in gene organization at a non-
                                                                                                                                                                           Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I: Lamiales: Orobanchaceae: Epifagus. NCBI_TaxID-4177:
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Pred. No. 1.4e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-93066301; Pubmed-1332054;
Wolfe K.H., Morden C.W., Palmer J.D.;
"Function and evolution of a minimal plastid genome from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: X61368; CAA43644.1; ·.
EMBL: M81884: AAA58870.1; ·.
PIR: S16720: S16720.
PIR: S20614: S20614.
Mendel: 5139: EPIVI:ycfl:1.
Chloroplast: Hypothetical protein.
SEQUENCE 1738 AA; 208318 MW; 65c63F63BDC8364B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nonphotosynthetic parasitic plant.";
Proc. Natl. Acad. Sci. U.S.A. 89:10648-10652(1992).
                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
ACMUC-2010 (Rel. 40, Last annotation update)
HYPOTHETICAL 208 KDA PROTEIN YCFI (ORF 1718).
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  PRT; 1738 AA
                                                                                                                                                Epiragus virginiana (Beechdrops).
Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Red clover mottle virus (RCMV).
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                                                                                                                                                                                                                                                                                                                                                                                                                               bioenergetic locus.";
J. Mol. Biol. 223:95-104(1992).
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75.0%;
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    STANDARD;
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Best Local Similarity
Matches 6; Conserv
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P35930;
  YCF1_EPIV1
000383;
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
V-TYPE ATP SYNTHASE SUBUNIT F (EC 3.6.1.34) (V-TYPE ATPASE SUBUNIT F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEMBRANE-BINDING PROTEIN (POTENTIAL).
VPG PROTEIN (POTENTIAL).
PROTEASE (POTENTIAL).
RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
       Shanks M., Lomonossoff G.P.; "The nucleotide sequence of red clover mottle virus bottom component RNA.";
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Archaea, Crenarchaeota, Desulfurococcales, Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyprotein; Transmembrane; Hydrolase; Protease; Transferase; RNA-directed RNA polymerase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97320421: Pubmed-9177272;
Shibui H., Hamamoto T., Yohda M., Kaqawa Y.;
"The stabilizing residues and the functional domains in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEASE COFACTOR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1; Length 186 pred. No. 1.5e+02; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL).
THIOL PROTEASE (POTENTIAL).
THIOL PROTEASE (POTENTIAL).
THIOL PROTEASE (POTENTIAL).
WW. 8DDD9D6C17C2B154 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR000605; RNA_helicase.
Interpro; IPR001205; RNA_pol_P3D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; PF00680; RNA_dep_RNA_pol; 1.
Pfam; PF00910; RNA_helicase; 1.
MEDLINE=93019077; Pubmed-1402822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.0%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X64886; CAA46104.1; -.
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483 499
983 98
1019 101
1109 110
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MEROPS; C03.003; -.
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927 YRYKNVPLTR 936
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MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., ClayLon R.A., Kirkness E.F.,
Kerlavage A. R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
Kerlavage A. R., Bult C.J., Tomb W., Fields C.A., Gocayne J.D.,
Koctt J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedbloum E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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Bacteria: Proteobacteria: gamma subdivision: Pasteurellaceae:
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.0%; Score 31; DB 1; Length 201; 50.0%; Pred. No. 22; tive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                           Score 31; DB 1; Length 102;
Pred. No. 11;
2; Mismatches 1; Indels
                                                                                                                                                                                    Hydrolase, ATP synthesis; Hydrogen ion transport.
SEQUENCE, 102 AA: 11499 MW; 4B0DE0FEBFDADF5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 201 AA; 23567 MW; 87964F8E43B4327B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Lasť sequence update)
04-NG-2001 (Rel. 40, Lasť annotation update)
HYPOTHETICAL PROTEIN HI1418.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 AA.
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                                                                                                          EMBL: U96487; AAB64415.1; --
InterPro; IPR002841; ATP-synt_F.
Pfam; PF01990; ATP-synt_F; 1.
ProDom; PD003811; ATP-synt_F; 1.
                                                                                                                                                                                                                                                       62.0%;
62.5%;
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Best Local Similarity 50.05
These 4; Conservative
                                                                                                                                                                                                                                                         Query Match 62.0
Best Local Similarity 62.5
Matches 5; Conservative
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24 YAFEDTPL 31
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ID YE18_HAEIN
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Db 23 FNFKDLPV 30
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1 YSFKDMPL 8

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Search completed: February 27, 2002, 11:42:41 Job time: 540 sec

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GenCore version 4.5
Copyright (c) 1993 · 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 27, 2002, 11:50:01 ; Search time 281.76 Seconds
(without alignments)
5.191 Million cell updates/sec Run on:

US-09-446-109A-3

1 YSFKDMPLXR 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues Searched: 473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_17:*

1: sp_archea:*
2: sp_bocteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:* sp_rodent:*
sp_virus:*
sp_vertebrate:* sp_organelle:* sp_phage:* sp_plant: * sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

		ď			SUMMARIES	
Result		Query	Query			
Q	Score	Match	Length	60	01	Description
-	38	76.0	1492	10	Q9FHA3	Q9tha3 arabidopsis
~	36	72.0	521	4		Q15725 homo sapien
٣	36	72.0	521	1	09лнсв	Q9jhc8 mus musculu
4	36	72.0	533	4	015724	Q15724 homo sapien
S	36	72.0	533	11	09JHC7	09jhc7 mus musculu
ø	36	72.0	581	4	Q15723	Q15723 homo sapien
7	36	72.0	581	11	Q9JHD0	Q9jhd0 mus musculu
æ	36	72.0	593	11	Q9JIIC9	Q9jhc9 mus musculu
6	36	72.0	914	6	Q9xJB1	Q9xjbl streptococc
9	36	72.0	1276	6	064284	064284 streptococc
=	36	72.0	1291	6	064295	064295 streptococc
7	35	70.0	175	7	092611	Q9z6il borrelia tu
13	35	70.0	473	7	Q9XA26	Q9xaz6 neisseria m
14	35	70.0	489	7	Q9K091	Q9k091 neisseria m
2	34	68.0	247	Ξ	Q9DAG5	Q9dag5 mus musculu
91	34	68.0	555	10	023360	023360 arabidopsis
17	34	68.0	999	7	P71093	P71093 bacteroides
81	34	68.0	1.117	7	053971	Q53971 streptococc
19	34	68.0	1579	S	Q9GRT7	Q9grt7 leishmania

099042 staphylococ 092311 rattus norv 094633 mus musculu 099139 mus musculu 099139 mus musculu 099472 staphylococ P93762 chondrus cr 045531 bacillus sp 77621 bradyrhitzob 09hef9 neurospora 062074 caenorhabdi 09hef9 neurospora 062074 caenorhabdi 09hef9 sugar beet 099703 beet yellow 099900 staphylococ 995667 clostridtum 045766 caenorhabdi 066182 read closuridtum 045766 caenorhabdi	P71102 curtobacter P87230 schizosacch O38728 bacteriopha	O9yh25 brachydanio Q9yh24 brachydanio Q9eqyl rattus norv Q9lgOl arabidopsis
2 099VH2 11 090CS3 11 090LS9 2 099V72 2 099V72 2 045531 2 045531 2 040521 2 090EF9 5 062074 2 099EF9 12 099F67 2 099V02 2 099V02 2 099V02 3 06567	T T O	13 Q9YH25 13 Q9YH24 11 Q9EQY1 10 Q9LG01
206 373 373 373 373 373 520 520 511 1151 1151 1151 3090 1180 1180 1180 1180 1180 1180 1180 1		435 490 524 526
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	644.0 64.0 64.0 64.0	64.0 64.0 64.0 64.0
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ALIGNMENTS

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Gaps .; 0 Length 1492; 1; Indels Score 38; DB 10; Pred. No. 32; 0; Mismatches 1 Query Match 76.0%; Best Local Similarity 87.5%; Matches 7; Conservative

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Created)
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SWART; SW00413; ETS. 1.
PROSITE; PS00345; ETS_DOMAIN_1: 1.
PROSITE; PS00346; ETS_DOMAIN_2: 1.
PROSITE; PS500361; ETS_DOMAIN_3: 1.
SEQUENCE 521 AA; 55733 MW; 6CA
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MEDLINE=96347578; Pubmed=8756667;
                                                                 MEDLINE-97154704; Pubmed-9001422;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00178; ELS; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
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Matches 6; Conserv
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Matches 6; Conserv
                                          SEQUENCE FROM N.A.
  NCBI_TaxID-10090;
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Q15724;
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Q15724
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MEDLINE-96347570: Pubmed-8756667:
OEttgen P., Akbarali Y., Boltax J., Best J., Kunsch C.,
Libermann T.A.;
"Characterization of NERF, a novel transcription factor related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97154704; PubMed-9001422; Wilkinson D.A., Neale G.A., Mao S., Naeve C.W., Goorha R.M.: "Elf-2, a rhombotin-2 binding ets transcription factor: discovery and potential role in T cell leukemia."; Leukemia 11:86-96(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Following FROM N.A.

SEQUENCE FROM N.A.

Wilkinson D.A., Neale G.A.M., Mao S., Fernandes E.R., Davenport J.W.,

Naeve C.W., Goorha R.M.;

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; U43189; AB37760.1; --

EMBL; AF256223; AAF67196.1; --

HSSP; P14921; 2STT.

InterPro; IPR000418; Ets.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
O
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                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NERF-1A--(ETS FAMILY TRANSCRIPTION FACTOR ELF2B).
NERF-1A--(ETS FAMILY TRANSCRIPTION FACTOR ELF2B).
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ETS FAMILY TRANSCRIPTION FACTOR ELE2B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 AA.
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85.7%; Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ets factor ELF-1.";
Mol. Cell. Biol. 16:5091-5106(1996)
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PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
SEQUENCE 521 AA; 56133 MW; AS44
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PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
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SEQUENCE FROM N.A.
                      11111 11
476 YSFKDRPL 483
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Libermann T.A.;
"Characterization of NERF, a novel transcription factor related to the
Ets factor ELF-1.";
Mol. Cell. Biol. 16:5091-5106(1996).
EMBL; U43189; AAB37761.1;
HSSP; P14921; 2STT.
Wilkinson D.A., Neale G.A., Mao S., Naeve C.W., Goorha R.M.; "Elf-2, a rhombotin-2 binding ets transcription factor: discovery and potential role in T cell leukemia."; Leukemia 11:86-96(1997).
                                                                                                                                       SEQUENCE FROM N.A.
Wilkinson D.A., Neale G.A.M., Mao S., Fernandes E.R., Davenport J.W.,
Naeve C.W., Goorha R.W.;
Submitted (ARR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF256218; AAF67193.1;
InterPro: IPR000418; Ets.
InterPro: IPR000431; HSF_ETS.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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85.7%; Pred. No. 27;
iive 0; Mismatches 1; Indels
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PROSITE: PS00346; ETS_DOMAIN_2; 1.
PROSITE: PS50061; ETS_DOMAIN_3; 1.
SEQUENCE 533 AA; 57388 MW; DAA5A5D12ECFD7E6 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Query Match
Best Local Similarity
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Submitted (Apr. 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; A7256219; AAF67194-1; --
InterPro: IPR000418; Ets.
InterPro: IPR00341; HSF_ETS.
                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuroynathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                    Wilkinson D.A., Neale G.A., Mao S., Naeve C.W., Goorha R.M.; "Elf-2, a rhombotin-2 binding ets transcription factor: discovery potential role in T cell leukemia."; Leukemia 11:86-96(1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Entoleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2001 (TrEMBLrel. 17, Last annotation update)
ETS TRANSCRIPTION FACTOR (ETS FAMILY TRANSCRIPTION FACTOR ELE2A)
NERF-2 OR ELF2.
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TISSUE-SPLEEN, FETAL LIVER, AND FETAL BRAIN;
MEDLINE-96347578; PubMed-8756667;
Oettgen P. Akbarali Y., Boltax J., Best J., Kunsch C.,
Libermann T.A.;
                                                                                                                                                                                                                                                                                                                                                                                                 778C30AB03AE0CD5 CRC64;
                                                                              01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ELFS FAMILY TRANSCRIPTION FACTOR ELF2B2.
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85.7%; Pred. No. 27;
Live 0; Mismatches 1;
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                                                           . 533 AA.
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Mol. Cell. Biol. 16:5091-5106(1996).
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PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
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Best Local Similarity
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1 YSFKDMP 7
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MEDLINE=97154704; PubMed=9001422; MEDLINE=97154704; PubMed=9001422; Wilkinson D.A., Neale G.A., Mao S., Naeve C.W., Goorha R.M.; "Elf.", a rhombotin-2 binding ets transcription factor: discovery and potential role in T cell leukemia."; Leukemia 11:86-96(1997).
         Wilkinson D.A., Neale G.A., Mao.S., Naeve C.M., Goorha R.M.; "Elf-2, a rhombotin-2 binding ets transcription factor: discovery and potential role in T cell leukemia."; Leukemia 11:86-96(1997).
                                                                                                                              SEQUENCE FROM N.A.
Wilkinson D.A., Neale G.A.M., Mao S., Fernandes E.R., Davenport J.W.,
Naeve C.W., Goorha R.M.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: U43188; AAB177591; ...
EMBL; AF256222; AAF67195.1; ...
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Mammalia; Euthazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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PROSITE; PS00346; ETS_DOMAIN_2: 1.
PROSITE; PS00061; ETS_DOMAIN_3: 1.
SEQUENCE 581 AA: 61933 MW; A39A8AB0170504ED CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ETS FAMILY TRANSCRIPTION FACTOR ELF2AL.
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30;
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Pred. No.
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85.7%; Pred. No.
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PROSITE; PS00346; ETS_DOMAIN_2: 1.
PROSITE; PS50061; ETS_DOMAIN_3: 1.
SEQUENCE 581 AA; 62711 MW; 5DS1
MEDLINE-97154704; Pubmed+9001422;
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InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
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85.7%;
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SMART; SM00413; ETS; 1.
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PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
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SEQUENCE FROM N.A.
MEDLINE=98160788; PubMed=9499809;
Desiere F., Lucchini S., Brussow H.;
"Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchanges followed by point mutations and small deletions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98160788; PubMed-9499809; Desiere F. Lucchini S., Brussow H.; Desiere F. Lucchini S., Brussow H.; Evolution of Streptococcus thermophilus bacteriophage genomes by modular exchanges followed by point mutations and small deletions and insertions."; Virology 241:345-356(1998).
EMBL: AFI15102. AAS39397. InterPro: IPR0000087; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus thermophilus bacteriophage Sfi21.
Viruses; dsDNA viruses, no RNA stage; Talled phages; Siphoviridae.
NCBL_TaxID=64186;
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Viruses; dsDNA viruses, no RNA stage; Talled phages; Siphoviridae.
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                                                                                                                                                           Length 914;
                                                  Tremblay D.M., Moineau S.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF085222; AAD21894.1; •.
SEQUENCE 914 AA: 103024 MW; 0C747BC05A3932C8 CRC64;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Pred. No. 72;
1; Mismatches
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49;
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EMBL; AF115103: AAC39283.1; -.
Interpror: IPRO00087; Collagen.
Hypothetical protein.
SEQUENCE 1276 AA: 142647 MW;
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75.0%;
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Best Local Similarity
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Matches 6; Conserv
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SEQUENCE FROM N.A.
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259 YSFKDSPM 266
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259 YSFKDSPM 266
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AF556217; AAR67192 l. .
MGD: MGI:1916507; 2610036A20Rik.
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     Gaps
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=97154704; PubMed=9001422; Wilkinson D.A., Neale G.A., Mao S., Naeve C.W., Goorha R.M.; Wilkinson D.A., a rhombotin-2 binding ets transcription factor: discovery potential role in T cell leukemia."; Leukemia 11:86-96(1997).
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Pred, No. 30;
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"Complete genomic sequence of the lytic bacteriophage Dfl
"treptococcus thermophilus.";
Virology 255:63-76(1999).
   Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ETS FAMILY TRANSCRIPTION FACTOR ELF2A2.
2610036A1V REFE2.
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1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PUTATIVE TAIL-HOST SPECIFICITY PROTEIN.
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 Mismatches
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PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
SEQUENCE 593 AA; 63202 MW; AGE
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Interpro; IPR002341; HSF_ETS.
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85.7%;
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SMART; SMO0413; ETS; 1.
6; Conservative
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Best Local Similarity
5, Conserva
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287 YQFKDMP 293
                                1 YSFKDMP 7
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09JHC9;
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55108 MW; 29E93256C94B9995 CRC64;

473 AA;

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SEQUENCE
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"Interplasmidic arm duplications determine virulence phenotype of the
bacterium Borrelia turicatae.";
Submitted (FEB-1998) to the EMBL/GenBank/DDDJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pennington P.M., Cadavid D., Bunikis J., Norris S., Barbour A.G.;
"Extensive interplasmidic duplications change the virulence phenotype of the relapsing fever agent Borrelia turicatae.";
MOI. Microbiol. 43:1120-1132(1999).
EMBL: AF0498652; AAD15784.1;
EMBL: AF129434; AAF34130.1;
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"Restriction barrier for transformation in Neisseria meningitidis.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ132413; CAB51246.1; -
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                                               571F36855F97B34F CRC64;
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SEOUENCE 175 AA; 20499 MW; AB03B55BC63F17E9 CRC64;
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01-MAY-1999 (TrEMBLrcl. 10, Created)
01-MAY-1999 (TrEMBLrcl. 10, Last sequence update)
01-MCT-2000 (TrEMBLrcl. 15, Last annotation update)
HYPOTHETICAL 20.5 KDA PROTEIN.
Borcrila turicatae.
Bacteria: Spirochaetales; Spirochaetaceae; Borrelia.
NCBI_TAXID-142;
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Last annotation update)
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                                                                                                            6
                                                                                                          Score 36; DB 9
Pred. No. 73;
1; Mismatches
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Pfam; PF01391; Collagen; 1.
Hypothetical protein.
SEQUENCE 1291 AA; 144338 MW;
                                                                                                          72.0%;
75.0%;
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                                                                                      Ouery Match
Best Local Similarity 75.0.
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Matches 6; Conservative
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Bacteria; Proteobacter
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259 YSEKDSPM 266
                                                                                                                                                                                          1 YSFKDMPL 8
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092611
1D 092611
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AC 092611
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OT 01-MAY
DT 01-CT

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MEDLINE-2017575; PubMed-10710307;

PELELIN H., Saunders N.J., Heldelberg J., Jeffries A.C., Nelson K.E., Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy K., Pererson J.D., Hickey E.K., Haft D.H., Salzberg S.L., Whiteo, Felsischmann R.D., Dougherty B.A., Mason T., Clecko A., Parksey D.S., Blair E., Citcone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamalhevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Vonter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis (serogroup B).
Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
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Mammalia, Euijoria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TYPE II RESTRICTION ENZYME HGAI.
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Pred. No. 40;
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                        DB
38;
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                        Score 35;
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MEDLINE-21085660; PubMed-11217851;
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75.0%;
                        70.0%;
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EMBL; AE002427; AAF41139.1;
TIGR: NMB0726; -.
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                    Conservative
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Best Local Similarity
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SEQUENCE 489 AA;
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267 YSFSEMPL 274
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A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Addota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,
A Redota K., Matsud H.A., Ashburner M., Batalov S., Casawant T.,
A Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
A Schriml L.M., Staubli F., Suzuki R., Tomita N., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiga M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordonei P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
A Winshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.",
Mature 409:685-690(2001).
EMBL; AK005861: BAB2-4381.1:
MGD; MGI:1922717; 1700011E24Rik.
SEQUENCE 247 AA: 27631 MW; 5A9BBD78EE7BB9FA CRC64;
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Best Local Similarity 85.7'
Matches 6; Conservative
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1 YSFKDMP 7 ||||| | 116 YSFKDKP 122

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Sequence Sequence

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Sequence 1 Sequence 1 Sequence 2

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Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database :

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APPLICANT: Standerson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Sterman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 1; Length 10; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Dann, Dorfman, Herrell and Skillman: 1601 Market Street Suite 720 Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                        US-08-299-285-6
US-08-299-285-8
US-08-299-285-8
US-08-299-285-18
US-08-299-285-28
US-08-299-285-28
US-08-299-285-29
US-08-299-285-29
US-08-299-285-39
US-08-299-285-31
US-08-299-285-31
US-08-299-285-31
US-08-985-126-16
PCT-US95-11126-15
PCT-US95-11126-16
                                                                                                                                                                                                                                                                                                                                              PCT-US95-11126-37
                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT AFFLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (215) 563-4100
TELEERX: (215) 563-4104
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08299285; Patent No. 5696230; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.0%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-299-285-7
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    RESULT
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1.702 Million cell updates/sec
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Sequence 7, Ap
Sequence 10, A
Sequence 5, Ap
Sequence 5, Ap
Sequence 5, Ap
                                                                                                                                          Search time 132.19 Seconds
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Sequence
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.: /cgn2_E/ptodata/2/iaa/5A_COMB.pep:*

.: /cgn2_E/ptodata/2/iaa/5B_COMB.pep:*

.: /cgn2_E/ptodata/2/iaa/6A_COMB.pep:*

.: /cgn2_E/ptodata/2/iaa/BECOMB.pep:*

.: /cgn2_E/ptodata/2/iaa/PCTUS_COMB.pep:*

.: /cgn2_E/ptodata/2/iaa/pcTUS_COMB.pep:*

.: /cgn2_E/ptodata/2/iaa/pcTUS_COMB.pep:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-995-126-7

US-08-995-126-7

US-08-995-11126-10

PCT-US95-11126-10

US-08-299-285-13

US-08-995-126-5

US-08-995-126-5

US-08-995-126-13

US-08-995-126-13

US-08-995-126-14

US-08-995-126-14

US-08-995-126-14

US-08-995-126-14

US-08-995-126-12

US-08-995-126-12

US-08-995-126-12

US-08-995-126-12

US-08-995-126-12

US-08-995-126-13

US-08-995-126-13

US-08-995-285-11

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r-us95-11126-19
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                                                                                                                                             February 27, 2002, 11:36:02
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                     length: 0
length: 200000000
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Result

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US-08-985-126-10
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APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.0%; Score 49; DB 1; Length 10; 90.0%; Pred. No. 0.00023; ive 0; Mismatches 1; Indels
   Indels
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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 Mismatches
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FILING DATE: 31-AUG-1994
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY MEET INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4104
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                   Sequence 10, Application US/08299285 Patent No. 5696230 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08985126 Patent No. 5942599
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FRAGMENT TYPE: C-terminal
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not relevant
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LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 90.0
Matches 9; Conservative
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          RY: US
19103-2307
                                     1 YSFKDMPLXR 10
                                                                         1 YSFKDMPLAR 10
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                                                                                                                                 RESULT 2
US-08-299-285-10
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US-08-985-126-7
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Matches
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Sequence 10, Application US/08985126
Patent No. 594259
GENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affairty Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESSONDENCE ADDRESS.
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
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STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 49; DB 2; I Pred. No. 0.00023; 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NIMBER: 63075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: No. 5942599 Relevant
TOPOLOCY: No. 5942599 Relevant
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.0%;
90.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 10 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                      STREET: 1601 Market
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YSFKDMPLXR 10
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US-08-985-126-7
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Sequence 10, Application PC/TUS9511126
GENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF ENVENTION: CTerminal Analogs of C5a Anaphylatoxin NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C.
STREET: 1601 Market Street Suite 720
CTTY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1..0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DB 5;
Pred. No. 0.00023;
0; Mismatches 1
                  APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
                                                                                              NAME: Reed, Janet E. RECISTRATION UNDBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                       SS: not relevant
not relevant
                                                                                                                                                                                                TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.0%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal
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Best Local Similarity 90.0

Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide HYPOTHETICAL: NO
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: not
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ZIP: 19103-2307
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APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCES: 37
CORRESPONDENCES: Dann, Dorfman, Herrell and Skillman, P.C.
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 2; Length 10;
Pred. No. 0.00023;
0; Mismatches 1; Indels
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                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
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                                                                                                                                                                                                     CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/299,285
FILING:DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: 63075
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4100
TELEPRAX: (215) 563-4100
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GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: No. 5942599 Relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO NTI-SENSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
                        COMPUTER READABLE FORM:
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ZIP: 19103-2307
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PCT-US95-11126-7
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APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.0%; Score 48; DB 1; Length 10; 90.0%; Pred. No. 0.00037; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUNESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720 CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "D-Phenylalanine at
position 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/299,285 FILING DATE: 31-AUG-1994 CLASS.FICATION: 530 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                    Sequence 13, Application US/08299285 Patent No. 5696230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Reed, Janet E. REGISTARTION UNBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-985-126-5; Sequence 5, Application US/08985126; Patent No. 5942599; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: not relevant not relevant
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TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 13
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Matches 9; Conservative
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ZIP: 19103-2307
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: no
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                                    1 YSFKDMPLXR 10
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APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                            ; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /product- "D-Alamine at position 9"
PCT-US95-11126-10
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2 IP: 19103-2307

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILIBLE
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
FLING DATE: 31-AUG-1994
CLASSIFICATION 1040BRRTON:
ATTORNEY/AGENT INFORMATION:
NAME: REGGY Janet E.
REGISTRATION NUMBER: 36,252
REGISTRATION NUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Denn, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                Score 49; DB 5; Pred. No. 0.00023; 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                98.0%;
90.0%;
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                  C-terminal
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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STRANDEDNESS: not
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                                                                                                                                                  FRAGMENT TYPE:
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US-08-299-285-5
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I.BM PC compatible
                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4004
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
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                                       Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 10 amino acids
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Best Local Similarity 90.0
Matches 9; Conservative
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ZIP: 19103-2307
COMPUTER READABLE FORM:
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OTHER INFORMATION:
US-08-985-126-13
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ZIP: 19103-2307
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ANTI-SENSE: NO
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                                       MEDIUM TYPE:
                                                                                                                                                        FILING DATE:
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Patent No. 594259
CENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Transky, Leonid
APPLICANT: Transky, Leonid
APPLICANT: Transky, Leonid
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                   APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96.0%; Score 48; DB 2; Length 10; 90.0%; Pred. No. 0.00037; Live 0; Mismatches 1; Indels
                                                                                                       ...orkSSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 63075
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPKX: (215) 563-4100
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SS: No. 5942599 Relevant
No. 5942599 Relevant
                                                                                                                                                                                                                                COUNTRY: 0S
2.1P. 19103-2307
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
Sanderson, Sam D.
Sherman, Simon A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.0
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: No. 5942599
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid STRANDEDNESS: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YSFKDMPLXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç
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: FRAGMENT TYPE:
US-08-985-126-5
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APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 48; DB 2; Length 10;
Pred. No. 0.00037;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C. STREET: 1601 Market Street Suite 720 CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "D-Phenylalanine at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: No. 5942599 Relevant
TOPOLOGY: No. 5942599 Relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 5, Application PC/TUS9511126 ; GENERAL INFORMATION:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                        NAME: Reed, Janet E. REISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
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Gaps
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APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarrsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SRQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    96.0%; Score 48; DB 5; Length 10; 90.0%; Pred. No. 0.00037;
                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                    OTHER INFORMATION: /product= "D-Phenylalanine at OTHER INFORMATION: position 9" PCT-US95-11126-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: "Alentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street Suite 720 CITY: Philadelphia STATE: PASTE: U.S. 21P: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: Rect TRAILOR NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08299285 Patent No. 5696230
                                                                                                         ANTI-SENSE: NO FRAGMENT TYPE: C-terminal COTGINAL SOURCE: ORGANISM: C5a Anaphylatoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                      STRANDEDNESS: not relevant
TOPOLGGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
                                                                                                                                                                                                                  NAME/KEY: Modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                    Query Match 96.0
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YSFKDMPLXR 10
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                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-299-285-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sancherson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Transfer, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF SEQUENCES: 37
OORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman, P.C.
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 48; DB 5; Length 10;
Pred. No. 0.00037;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION.

PRIOR APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E. REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4104
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/11126
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                    NAME: Reed, Janet E. REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-404
INFORMATION FOR SEQ ID NO: 5: SEQUENCE:CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 13, Application PC/TUS9511126
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: FIB PC compatible
                                                                                                                                                                                                                                                                                                                         SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 96.0
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1601 Market
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YSFKDMPLXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                            HRAGMENT TYPE: PCT-US95-11126-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-11126-13
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RESULT 15
PCT-US95-11126-14
Squence 14, Application PC/TUS9511126
SGQUENCE 14, Application PC/TUS9511126
GENERAL INFORMATION:
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ОТНЕR INEURMATION: /product- "D-Proline at position 9"
PCT-US95-11126-14
                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C. STREET: 1601 Market Street Suite 720 STREET: Philadelphia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 47; DB 5;
Pred. No. 0.0006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: February 27, 2002, 11:36:02 Job time: 141 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Reed, Janet E. REISTRATION UNBER: 36,252
REFISENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.0
Matches 9. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YSFKDMPLXR 10
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                        1 YSFKDMPLXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NAMNT-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.0%; Score 47; DB 2; Length 10; 90.0%; Pred. No. 0.0006; Live 0; Mismalches 1; Indels
                                                                                                        Length 10;
                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
; LOCATION: 9; CTHER INFORMATION: "D-Proline at position 9" US-08-299-285-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 9
OTHER INFORMATION: "D-Proline at position 9"
                                                                                                        Score 47; DB 1;
Pred. No. 0.0006;
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DAIL.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGGET INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
; REFERENCE/OCKET NUMBER: 63075
; TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: No. 5942599 Relevant
TOPOLOCY: No. 5942599 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                           ; Sequence 14, Application US/08985126
; Patent No. 5942599
                                                                                                                                                0;
                                                                                                        94.0%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Modified-site
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                                                                                                      Query Match
Best Local Similarity 90.0
Matches 9: Conservative
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STRANDEDNESS: NO.
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Best Local Similarity
Matches. 9; Conserv
                                                                                                                                                                                           1 YSFKDMPLXR 10
                                                                                                                                                                                                               1 YSEKDMPLPR 10
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CSa anaphylatoxin CSa anaphylatoxin CSa anaphylatoxin CSa anaphylatoxin Arabidopsis thalia Arabidopsis thalia

AAG14717 AAG54216 AAB06071 AAB06070

AAR94482 AAR94478 AAR94479 AAG27308

Human protein sequ

AAG54215 AAB95561 AAR94489

AAR94490

AAR94493 AAR94494 AAR94495

AAR94496

AAR94497

C5a anaphylatoxin C5a anaphylatoxin C5a anaphylatoxin C5a anaphylatoxin C5a anaphylatoxin C5a analogue C5a(6 C5a anaphylatoxin C5a anaphylatoxin C5a anaphylatoxin C5a anaphylatoxin

AAR94498 AAR94499 AAR94500 AAR94471 AAR94480 Arabidopsis thalia Arabidopsis thalia Arabidopsis thalla Arabidopsis thalla

AAG08830 AAG08829

AAR94481

AAG08828

AAG4 327

ALIGNMENTS

RESULT

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(without alignments)
2.441 Million cell updates/sec
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                                                                                                        February 27, 2002, 11:41:13; Search time 303.5 Seconds
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                  Compugen Ltd.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
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AAW27256
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antigen presenting cell: APC; viral pathogen; and thumour response; antibody; immunodiagnostic; immunotherapeutic Molecular asjuvant; immune response; immunogen; binding affinity; Tempero RA; /note= "D-form residue" Molecular an invant targeting ligand. Location/Qualifiers AAW27250 standard; peptide; 10 AA. Hollingsworth MA, Sanderson SD, 95US-0005727 96WO-US16825 (first entry) (UYNE-) UNIV NEBRASKA WPI; 1997-244854/22. Misc-difference 18-OCT-1996; 20-OCT-1995; WO9714426-A1 23-DEC-1997 24 - APR - 1997 Synthetic AAW27250; AAW27250 Molecular adjuvant Molecular adjuvant Molecular adjuvant GSa anaphylatoxin CSa anaphylatoxin CSa anaphylatoxin CSa anaphylatoxin CSa anaphylatoxin CSa anaphylatoxin CSa anaphylatoxin

AAR94468 AAR94486 AAR94477

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WPI; 1997-244854/22.
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                                                                  response to an immunogen. The molecular adjuvant comprises a targeting response to an immunogen. The molecular adjuvant comprises a targeting response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ligand being functionally linked to the immunogen and so binding of the molecular adjuvant to the APC; determinant activates the APC, effecting delivery of the APC; timmunogen to an antigen presenting pathway of the APC. The present sequence represents a specifically claimed targeting ligand, which is a C5a C-terminal decapeptide agonist. The molecular adjuvant can be used to produce an immune response for protecting against viral and other pathogens or to produce anti-tumur responses. It can also be used for the production of antibodies for use as immunodiagnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and provide for the production of antibodies against a weakly-antigenic or non-antigenic substances.
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Molecular adjuvants for enhancing immune responses - comprise an immunogen linked to a ligand having binding affinity for a determinant of an antigen presenting cell.
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                                                                                                                                                                                                                                                                                                        Score '50, DB 18; Length 10;
Pred. No. 0.0023;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aliphatic spacer moiety
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW27254 standard; peptide; 12 AA
                                                Claim 5; Page 51; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= OTHER
                                                                                                                                                                                                                                                                                                          98.0%;
90.0%;
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Best Local Similarity 90.0
Matches 9: Conservative
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Targana, maying untuing attituty to a characteristic decomposition of an antigen presenting cell (APC), the targeting ligand being functionally linked to the immunogen, and so binding of the molecular adjuvant to limber determinant activates the APC, effecting delivery of the person immunogen presenting pathway of the APC. The present sequence represents a specifically claimed formula for a molecular adjuvant, where the immunogen is serum amyloid A. The molecular adjuvant can be used to produce an immune response for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be immunotherapeutic agents. The molecular adjuvant is readily taken up and processed by APCs to provide APC-mediated immune responses. It can provide for the production of antibodies against a weakly-antigenic or
                                                                                                                                                                                                                   A novel molecular adjuvant has been developed for enhancing an immune response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an
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Molecular adjuvants for enhancing immune responses - comprise an immunogen linked to a ligand having binding affinity for a
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                                                                           determinant of an antigen presenting cell
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                                                                                                                                               Claim 15; Page 53; 61pp; English.
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Matches 9; Conservative (
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                                                     response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ligand being functionally
                                                                                    linked to the immunogen, and so binding of the molecular adjuvant to the APC determinant activates the APC, effecting delivery of the immunogen to an antigen presenting pathway of the APC. The present sequence represents a targeting ligand and immunogen, in which the juxa-membrane epitope of human mucin-1 is positioned toward the carboxyl terminus and the C5a analogue is positioned toward the terminus. The molecular adjuvant can be used to produce an immune
                                           A novel molecular adjuvant has been developed for enhancing an immune
                                                                                                                                                                response for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiagnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and processed by APCs to provide APC-madaiated immune responses. It can provide for the production of antibodies against a weakly-antigenic or
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular adjuvant; immune response; immunogen; binding affinity; antigen presenting cell; APC; viral pathogen; anti tumour response; antibody; immunodiagnostic; immunotherapeutic; agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular adjuvants for enhancing immune responses - comprise an immunogen linked to a ligand having binding affinity for a determinant of an antigen presenting cell
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                                                                                                                                                                                                                                                                                           Score 50; DB 18; Length 18; Pred. No. 0.0041;
                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecular adjuvant targeting ligand and immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tempero RA;
                                                                                                                                                                                                                                                                                                                 0; Mismatches
 determinant of an antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
18
                      Example 1; Page 31; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 AAW27251 standard; peptide; 19 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hollingsworth MA, Sanderson SD,
                                                                                                                                                                                                                                                                                           98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96WO-US16825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1997 (first entry)
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0
                                                                                                                                                                                                                                      non-antigenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNE-) UNIV NEBRASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-244854/22
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                                                                                                                                                                                                                                                            18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW27251;
                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ligand being functionally linked to the immunogen, and so binding of the molecular adjuvant to the APC determinant activates the APC, effecting delivery of the immunogen to an antigen presenting pathway of the APC. The present sequence represents a specifically claimed targeting ligand and immunogen. The molecular adjuvant can be used to produce an immune response for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiagnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and processed controlled to production of antibodies against a weakly-antigenic or
                                                                 novel molecular adjuvant has been developed for enhancing an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune adjuvant; immunodeficiency; augmentation; immune therapy;
cancer; drug delivery; ONS disorder; central nervous system;
Alzheimer's disease; tumour; high affinity; reseptor antagonist;
development; non-steroidal; anti-inflammatory.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C5a anaphylatoxin analogue C5a(65-74) Tyr65 Pro69 D-Ala73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50; DB 18; Length 19; pred. No. 0.0044; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taylor SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sherman SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "D-form residue"
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10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR94487 standard; peptide; 10 AA
Claim 6; Page 52; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0299285.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US11126
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-antigenic substances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UYQU ) UNIV QUEENSLAND.
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                                                                                                                                        region from human CSa anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible c-terminal region) comprising a beta-turn. Analoques with type (II or V) and type III beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (especifically vascular) wascular) permeability, respectively.
                                                                                                                                                                                                                                                                                                          The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeablility, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develophigh affinity C5a receptor antagonists useful as non-steroidal
                 C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; druq delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                            present peptide is an analogue of a C-terminal decapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constrained backbone conformation; proinflammatory response; spasmogenesls; platelet aggregation; neutrophil; non-mediated; mediated; increase; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSa anaphylatoxin C-terminal analogue C5a(65-74) Tyr65 Ala73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 17; Length 10; Pred. No. 0.074; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-terminal; human; C5a anaphylatoxin; analogue; beta-turn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          development; non-steroidal; anti-inflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                        Claim 8; Page 88; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.4%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-inflammatory agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 80.0
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YSFKPMPLXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 AA;
                                                     permeability
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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C5a anaphylatoxin C-terminal analogue C5a(65-74) Tyr65 Pro71 D-Ala73.
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                                                                                                                                                                                                                                         The present peptide is an analogue of a C-terminal decapeptide region from human C5a anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with type (II or V) and type III beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (esp.
                                                                                                                        C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C-terminal; human; C5a anaphylatoxin; analogue; beta-turn; constrained backbone conformation; proinflammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated; mediated; increase; cell membrane; vascular; permeabilitty; neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunedeficiency; augmentation; immune therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      In a type (II or v) beta-turn specific human foetal artery smoot muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of 122 and 48, compared to 0.018 and 0.0013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.4%; Score 42; DB 17; Length 10; 80.0%; Pred. No. 0.074;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                          Sherman SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                    vascular) permeability, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                       Example 2; Page 79; 116pp; English.
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                                        Kirnarsky L, Sanderson DG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anti-inflammatory agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 80.0
Matches 8; Conservative
(UYQU ) UNIV QUEENSLAND.
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| ysfkdmplar 10
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mediated; increase; cell membrane; vascular; permeability;
                                                                                                                                                                                                                                                                                             Kirnarsky L,
                                                                               Homo sapiens
                                                                                                                                                                                                                 31-AUG-1995;
                                                                                                                                                                                                                                      31-AUG-1994;
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                                                                                                                                                                                                                                                                  The present peptide is an analogue of a C-terminal decapeptide region from human C5a anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with type (II or V) and type III beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme respectively.

The analogues can be used as immune adjuvants for the treatment of
                                                                                                                                                                                                    C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In a type (II or V) beta-turn specific human foetal artery smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microm) activities of 0.35 and 2.1, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders such as Alzheimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal anti-inflammatory agents.
                                                                                                                                                                                                                                                                                                                                                                                               immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C5a anaphylatoxin analogue C5a(65-74) Tyr65 Pro7l D-Phe73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 17; Length 10;
Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                          Taylor SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                          Sherman SA,
          /note= "D-form residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR94476 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                 Claim 8; Page 81; 116pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.4%;
80.0%;
                                                                                                                                                          Sanderson DG,
                                                                             95WO-US11126
                                                                                                  94US-0299285
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Best Local Similarity 80.v
                                                                                                                                    QUEENSLAND.
                                                                                                                        NEBRASKA
                                                                                                                                                                              WPI; 1996-160140/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA;
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                                                                                                                                                         Kirnarsky L,
                                                                            31-AUG-1995;
                                                                                                  31-AUG-1994;
                                WO9606629-A1
                                                                                                                                                                                                                            permeability
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                                                       07-MAR-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-terminal analogues of C5a anaphylatoxin · induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In a type (II or V) beta-turn specific human foetal artery smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders such as Alzheimer's disease or tumours, and to develop
high affinity C5a receptor antagonists useful as non-steroidal
neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor anteaponist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                         development; non-steroidal; anti-inflammatory.
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Pred. No. 0.11;
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                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Page 82; 116pp; English.
                                                                                                                                                                                                                                                                                                                                       /note= "beta-turn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.4%;
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QUEENSLAND
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The 8; Conserve
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lysfkdmplfr 10
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The present peptide is an analogue of a C-terminal decapeptide region from human C5a anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flaxible C-terminal region) comprising a beta-turn. Analogues with type (II or v) and type III beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophilon-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil engine release and neutrophil mediated increases in cell membrane (esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
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                                                                                                                                                                              constrained backbone conformation; proinflammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated; smediated; inforease; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders such as Alzheimer's disease or tumours, and to develop
high affinity C5a receptor antagonists useful as non-steroidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS
                                                                                                                                C5a anaphylatoxin C-terminal analogue C5a(65-74) Tyr65 Pro71.
                                                                                                                                                                  C-terminal; human; C5a anaphylatoxin; analogue; beta-turn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taylor SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vascular) permeability, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                 AAR94468 standard; peptide; 10 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanderson DG,
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                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-inflammatory agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-1994;
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                                                                                           17-OCT-1996
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                                                       AAR94468;
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AAR94468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vascular) permeability, respectively.

The analogues can be used as immune adjuvants for the treatment dimmune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal
                                                                                                                                                                                                                                                                                                                                                           spasmogenesis; platelet aggregation; neutrophil; non-mediated; mediated; increase; cell membiates; vacular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzheimer's disease; trmour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
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                                                                                                                                                                                                                                                                                                                                             constrained backbone conformation; proinflammatory response;
                                                                                                                                                                                                                                                                                                                           human; C5a anaphylatoxin; analogue; beta-turn;
 ich 10;
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                                                                                                                                                                                                                                                                                           CSa anaphylatoxin analogue CSa(65-74) Tyr65 Gly69 Pro70.
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DB 17
Score 41; DB 17
Pred. No. 0.11;
0; Mismatches
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                                                                                                                                                                                      AAR94486 standard; peptide; 10 AA.
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80.4%;
80.0%;
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                                                                  1 YSFKPMPLXR 10
                                                                                     Kirnarsky L,
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Query Match
Best Local E
Matches 8,
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characterised by spasmogenesis, platelet aggregation and neutrophil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region from human C5a anaphylatoxin, which has a constrained backhone conformation (compared to the natural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with type (II or V) and type III beta-turns elicit proinflammatory responses
anti-inflammatory agents.

In a type (II or V) beta-turn specific human foetal artery smooth muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of 0.59 and 2.0, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                     C-terminal; human; C5a anaphylatoxin; analogue; beta-turn; constrained backbone conformation; proinflammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated; mediated; locrease; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant; immunodeficiency; augmentation; immunot therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist;
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                                                                                                             DB 17; Length 10;
                                                                                                                                   2; Indels
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                                                                                                                      Pred. No. 0.18;
0; Mismatches
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                                                                                                             Score 40;
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                                                                                                           78.4%;
80.0%;
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Matches ::8; : Conservative
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                                                                                                             Query Match
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The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune the therapy for the treatment of cancer, without inflammatory side ceffects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop in the finity. CS receptor antagonists useful as non-steroidal anti-inflammatory agents.

In a type (II or V) beta-turn specific human foetal artery smooth muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective ECSO (microM) activities of 3.7 and 2.5, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; drug delivery; ONS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C5a anaphylatoxin analogue C5a(65-74) Tyr65 Pro71 Ala72 D-Ala73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-terminal: human; CSa anaphylatoxin; analogue; beta-turn; constrained backbone conformation; proinflammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated; mediated; increase; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 17; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 17
Pred. No. 0.18;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherman SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note*."D-form residue"
                                                                                               vascular) permeability, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR94475 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.4%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95WO-US11126.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYNE-) UNIV NEBRASKA.
(UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
England 8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YSFKPMPLXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ysfkdmplpr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
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us-09-446-109a-4.rag

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                                                                                                                                               region from human CSa anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible c-terminal region) comprising a beta-turn. Analogues with type (II beta-turns elicit proinflammatory responses) constrained by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically wascular) permeability, or neutrophil mediated increases in cell membrane (esp. vascular) permeability, respectively.

The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS increasing vascular permeability, e.g. in the treatment of CNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
            C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane permeability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C5a anaphylatoxin C-terminal analogue C5a(65-74) Tyr65 Pro71 Ala72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In a type (II or V) beca-turn specific human foetal artery smooth mascle confraction assay, and a type III beta-turn specific neurophil polarisation assay the peptide had respective EC50 (microM) activities of 17.9 and 5.6, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal; human; C5a anaphylatoxin; analogue; beta-turn; constrained backbone conformation; prointlammatory response; spasmogenesis; platelet aggregation; neutrophil. non-mediated; mediated; increase; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immunodeficiency; augmentation; immune therapy; cancer; drug delivery; CNS disorder; central nervous system: Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders such as Alzheimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal
                                                                                                                                   The present peptide is an analogue of a C-terminal decapeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
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0; Mismatches
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                                                                                             Example 2; Page 66; 116pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "beta-turn"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-inflummatory agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YSFKPMPLXR 10
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| ysfkdmpaar 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 AA;
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region from human C5a anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible C-terminal region) comprising a beta-turn. Analogues with type C-terminal region comprising a beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil energine release and neutrophil mediated increases in cell membrane (csp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vascular) permeability, respectively.

The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affairty GSa receptor antagonists useful as non-steroidal anti-inflammatory agents.
                                                                                                                                                                                                               C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In a type (If or V) beta-turn specific human foetal artery smooth mascle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of >1000 and 215, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune adjuvant; immunodeficiency; augmentation; immune therapy; cancer; frug delivery; CNS disorder; central nervous system; Alzheimer's disease; tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C5a anaphylatoxin analogue C5a(65-74) Tyr65 Ala70 Pro71 D-Ala73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                           present peptide is an analogue of a C·terminal decapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-terminal; human; C5a anaphylatoxin; analogue; beta-turn; constrained backbone conformation; prointlammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated; mediated; increase; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                        Taylor SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                        Kirnarsky L, Sanderson DG, Sherman SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.6%; Score 36;
70.0%; Pred. No. 1
                                                                                                                                                                                                                                                                                                   Example 2; Page 81; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR94482 standard; peptide; 10 AA.
95WO-US11126
                                     94US-0299285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                  OUEENSLAND.
                                                                             (UYNE-) UNIV NEBRASKA
                                                                                                                                                                              WPI; 1996-160140/16
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31-AUG-1995;
                                     31-AUG-1994;
                                                                                              (UYQU ) UNIV
                                                                                                                                                                                                                                                              permeability
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mediated; increase; cell membrane; vascular; permeability; neutrophil polarisation; neutrophil enzyme release; treatment; immune adjuvant. Immunodeficiency; augmentation; Immune therapy; cancer; drug delivery; CNS disorder; central nervous system; Alzheimer's disease, tumour; high affinity; receptor antagonist; development; non-steroidal; anti-inflammatory.
                          C-terminal; human; C5a anaphylatoxin; analogue; beta-turn; constrained backbone conformation; proinflammatory response; spasmogenesis; platelet aggregation; neutrophil; non-mediated;
  C5a anaphylatoxin analogue C5a(65-74) Tyr65 Ala70 Pro71.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-160140/16.
                                                                                                                                                                                                                                                                                                                                                                                         Kirnarsky L,
                                                                                                                                                                                                                                        WO9606629-A1.
                                                                                                                                                                                                                                                                                                                                                (UYNE-) UNIV
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                     31-AUG-1994;
                                                                                                                                                                                                                                                                                           31-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                region from human C5a anaphylatoxii, which has a constrained backbone conformation (compared to the natural peptide's flexible c-terminal region) comprising a beta-turn Analoques with type (II or V) and type III beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (esp. vascular) permeability, respectively.
                                                                                                                                                                                                                                                                                                      C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the treatment of cancer, without inflammatory side
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In a type (II or V) beta-turn specific human foetal artery smooth muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microm) activities of 0.33 and 2.3, compared to 0.018 and 0.0013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           effects. They can also be used to facilitate drug delivery by increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzbeimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                      present peptide is an analogue of a C-terminal decapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.6%; Score 36; DB 17; Length 10; 70.0%; Pred. No. 1; ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                     Taylor SM;
                                                                                                                                                                                                                                                     Sherman SA,
                                                                              /note= "D-form residue"
                          Location/Qualifiers
                                                  /note= "beta-turn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR94478 standard; peptide: 10 AA.
                                                                                                                                                                                                                                                                                                                                                            Claim 8; Page 85; 116pp; English.
                                                                                                                                                          95WO-US11126
                                                                                                                                                                                   94US-0299285
                                                                                                                                                                                                                                                   Sanderson DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (tirst entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-inflammatory agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 70.6
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                          (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                           NEBRASKA
                                                                                                                                                                                                                                                                            WPI; 1996-160140/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA;
                                                                Misc-difference
  Homo sapiens
                                                                                                                                                          31-AUG-1:995;
                                                                                                                                                                                                             (UYNE-) UNIV
                                                                                                                                                                                                                                                  Kirnarsky L,
                                                                                                                                                                                                                                                                                                                                   permeability
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                                       Reg ton
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Taylor SM;

Sherman SA,

Sanderson DC,

NEBRASKA. QUEENSLAND.

95WO-US11126. 94US-0299285

Location/Qualifiers /note= "beta-turn"

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                                                                                                                                                                                                                                                           region from human CSa anaphylatoxin, which has a constrained backbone conformation (compared to the natural peptide's flexible c-terminal region) comprising a beta-turn, Maloques with type creminal region) comprising a beta-turn analoques with type (II beta-turns elicit proinflammatory responses characterised by spasmogenesis, platelet aggregation and neutrophil non-mediated increases of cell membrane (specifically vascular) permeability, or neutrophil polarisation, neutrophil enzyme release and neutrophil mediated increases in cell membrane (esp. vascular) permeability, respectively.

The analogues can be used as immune adjuvants for the treatment of immune deficiency disorders, and for augmenting standard immune therapy for the Lreatment of cancer, without inflammatory side effects. They can also be used to facilitate drug delivery by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muscle contraction assay, and a type III beta-turn specific neutrophil polarisation assay the peptide had respective EC50 (microM) activities of 1.74 and 15.8, compared to 0.018 and 0.0013
C-terminal analogues of C5a anaphylatoxin - induce e.g. spasmogenesis, platelet aggregation and increases in cell membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 In a type (II or V) beta-turn specific human foetal artery smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           increasing vascular permeability, e.g. in the treatment of CNS disorders such as Alzheimer's disease or tumours, and to develop high affinity C5a receptor antagonists useful as non-steroidal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                    The present peptide is an analogue of a C-terminal decapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35;
Pred. No. 1
                                                                                                                                                         Claim 8; Page 83; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.68;
70.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .-inflammatory agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YSFKPMPLXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ysfkdaplyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA;
                                                                                  permeability
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Search completed: February 27, 2002, 11:41:13 Job time: 452 sec

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GenCore version 4.5
Copyright (c) 1993 · 2000 Compugen Ltd.
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 protein search, using sw model OM protein

Run on:

February 27, 2002, 11:45:13 ; Search time 145.23 Seconds (without alignments) 5.245 Million cell updates/sec

US-09-446-109A-4

1 YSFKPMPLXR 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 su

PIR_68:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	mid - niedocom	lpha reaul	HNF-3/forkhead pro	fork head-related	hypothetical prote	_	_	П	hypothetical prote	brobable tropinone	hypothetical prote	hypothetical prote	ت	RIC1 protein - yea	pr	probable mitochond	probable sugar nuc	hypothetical prote	_	hypothetical prote	hypothetical prote	response regulator	sulfite reductase	phosphotransferase	hypothetical prote		Ω	hypothetical prote	•
	10	JE0291	T48372	T42255	T42234	T37204	T23775	T27066	T27067	T27684	D84695	B70640	S59327	T19118	826039	G75378	S62485	T00613	G86832	T31919	F71422	C64502	T09113	S74718	00BEJ5	C86203	T49726	S52493	C71039	T41226
	DB	5	7	7	7	7	7	7	7	7	~	7	~	~	7	7	7	7	7	7	7	~	~	7	.	7	7	7	7	ç
	Length	940	495	510	530	622	9	717	717	2219	271	275	748	755	1056	183	271	278	319	426	468	505	584	635	707	860	1198	103	163	203
œ	Ouery Match	70.6	68.6	9.89	9.89	9.89	9.89	9.89	68.6	68.6	66.7	66.7	66.7	66.7	66.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	64.7	•	₹.	Ť.	Α.	ζ.	62.7	62 7
	Score	36	35	35	35	35	35			35						33	33	33	33		33									
	Result No.	-	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	hypothetical prote	R2R3-MYB transcrip	myb-related protei	probable ubiquinon	hypothetical prote	type I restriction	beta-glucosidase (middle T antiqen -	type II site-speci	sucrosefructan 6	hypothetical prote	cation efflux syst	hypothetical prote	genome polyprotein	cardiolipin syntha
S32963	T23319	T45859	S71285	T41372	E72672	C82516	GLJY14	TVVPM	A811'66	T06184	T24365	F70342	. 965058	JQ1895	B82724
7	~	~	П	7	7	7	1	-	7	7	7	~	~	7	7
232	277	301	304	305	346	424	425	440	489	625	619	1019	1430	3163	652
62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	8.19
32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	31.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5

FB19 protein - human C;Species: Homo sapiens (man) C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000

C;Accession: JE0291
R;Totaro, A.; Grifa, A.; Carella, M.; Rommens, J.M.; Valentino, M.A.; Roetto, A.; Zel
Biochem. Biophys. Res. Commun. 250, 555-557, 1998
A;Title: Cloning of a new gene (FR19) within HLA class I region.
A;Reference number: JE0291; MUID:99003493

A;Cross-references: GB:Y13247; NID:g2117158; PIDN:CAA73697.1; PID:g2117159 A; Molecule type: mRNA A; Residues: 1-940 <TOT>

A; Map position: 6p21.3

ö Gaps . 0 Score 36; DB 2; Length 940; pred. No. 43; 2; Mismatches 2; Indels 70.6%; Query Match 70.6 Best Local Similarity 60.0 Matches 6; Conservative

1 YSFKPMPLXR 10

1: 11:11 1 236 YNEKPIPEKR 245

AtB'alpha regulatory subunit of PP2A - Arabidopsis thaliana
NiAlternate names: protein F1284-340
G.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Sacession: T48172
C.Sacession: T48177
S. Weizeneger, T.: Bancroft, I.: Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, March 2000

A:Reference number: 224492 A:Accession: T48372 A:Status: preliminary

A; Molecule type: DNA

A:Residues: 1.495 <BEV>
A:Cross-references: EMBL:AL162751
A:Experimental source: cultivar Columbia; BAC clone F12E4

A: Map position: 5 A: Introns: 387/3 A: Note: F12E4.240

Score 35; DB 2; Length 495; Pred. No. 33; 68.6%; 60.0%; Query Match Best Local Similarity

```
A:Map position: 1
A:Introns: 214/3; 268/3; 329/2; 419/3; 457/2; 547/2; 563/1
A:Note: R.13H8.1
C:Superfamily: unassigned fork head proteins; fork head DNA-binding domain homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-717 - WHI.>
A.Status: 1-717 - WHI.>
A.Stross-references: EMBL.AL021493; PIDN:CAA16394.1; GSPDB:GN00023; CESP:Y51A2B.6a
A.Experimental source: clone Y51A2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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A;Molecule type: DNA
A;Residues: 1-690 <WIL>
A;Cross-references: EMBL:Z82278; PIDN:CAB05258.1; GSPDB:GN00023; CESP:M162.7
A;Experimental source: clone M162
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein M162.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T23775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Y51A2B.6a - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Introns: 37/1; 389/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Yll6ABC.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33
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                                A.Accession: T37204
A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-622 <WIL>
A.Cross-references: EMBL:AF039717; PIDN:AAB96741.1
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Basham, V. submitted to the EMBL Data Library, November 1996 A:Reference number: 219797 A:Accession: T23775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 2
Pred. No. 48;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, January 1998
A;Reference number: 220305
A;Accession: T27066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 68.6%;
Best Local Similarity 85.7%;
Matches 6; Conservative
   A; Reference number: 221633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP:Y51A2B.6a
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323 SFKPLPL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 5
A;Introns: 8/1; 33/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SFKPMPL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: CESP:M162.7
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R;McMurray, A.
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T27066
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C:Species: Caenorhabditis alegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
A:Title: The Fork head transcription factor DAF-16 transduces insulin-like metabolic and A:Reference number: 222108; MUID:98013175
A:Reference number: 222108; MUID:98013175
A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sp
                                                                                                                                                                                                                                                                                                                                               C; Species: Caenorhabditis elegans
C;Date: 03-bec-1999 | $sequence_revision 03-bec-1999 | $text_change 05-May-2000
C;Date: 03-bec-1999 | $sequence_revision 03-bec-1999 | $text_change 05-May-2000
C;Date: 03-1995 | $text_change 05-May-2000
C;Date: 03-bec-1999 | $text_c
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A:Gene: daf-16
C:Superfamily: unassigned fork head proteins: fork head DNA-binding domain homology
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A;Molecule type: mRNA
A;Residues: 1-510 <LIN>
A;Cross-references: EMBL:AF032112; NID:g2623942; PIDN:AAC47803.1; PID:g2623943
C;Genetics:
A;Gene: daf-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:AF020344; NID:q2618980; PIDN:AAB84392.1; PID:q2618981
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hypothetical protein R13HB.1 - Caenorhabditis elegans
hypothetical protein R13HB.1 - Caenorhabditis elegans
C:Species: Cacnorhabditis elegans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
C:Accession: T37204
R:Jones, K.; Hinds, K.; Sutterer, C.; Cofman, M.
Submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid R13HB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 510;
                                                                                                                                                                                                                                                                                                                  HNF-3/forkhead protein homolog daf-16 - Caenorhabditis elegans
   Indels
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   5
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Pred. No. 34;
1; Mismatches
   Mismatches
   5
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85.7%;
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Best Local Similarity 85.77
The 6: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 68.6
Best Local Similarity 85.7
Matches 6; Conservative
Conservative
                                                                                                         11 :1:11 1
67 YSVEPLPLFR 76
                                                                     1 YSFKPMPLXR 10
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A; Residues: 1-530 <OGG>
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417 NFKPMPL 423
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   . 9
   Matches
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Query Match

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Chacession: B7060

B;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Condon, R.; Barcer, B.; Davies, B.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Sulscon, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Tille: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987

A;Reference number: A70500; MUID:98295987

A;Residues: 1-275 con.>
A;Residues: 1-275 con.>
A;Residues: 1-275 con.>
A;Cross-references: GB:Z84395; GB:AL123456; NID:93261698; PIDN:CAB06450.1; PID:918061
                                                                                                   Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benilo, M.L.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talixii, euss. D.; Nerman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; VanLer Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Recession: D84695
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Gene: Rv0687
C.Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;11-204/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 2
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-references: GB:AE002093; NID:93980399; PIDN:AAC95202.1; GSPDB:GN00139 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nypothetical protein YLR135w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L3140
C;Species: Saccharomyces cerevisiae
C;Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 29-Oct-1999
C;Accession: S59327; S64977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Rv0687 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
probable tropinone reductase [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress) C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C.Accession: D84695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34: DB 2; Length 271;
Pred. No. 27;
2; Mismatches 0; Indels
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Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: strain H37Rv
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Matches 6; Conservative
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A; Residues: 1-271 <STO>
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A:Introns: 139/3; 246/3; 487/3; 784/1; 960/2; 1067/3; 1113/3; 1171/3; 1321/2; 1383/3; 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Molecule type: DNA
A:Residues: 1-717 <WIL>
A:Cross-references: EMBL:AL021493; PIDN:CAA16395.1; GSPDB:GN00023; CESP:Y51A2B.6b
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A:Cross-references: EMBL:Z70038; PIDN:CAA93884.1; GSPDB:GN00020; CESP:ZK1067.2
                                                                                                                                                                                                                                                                           RESULT 8
T27067
hypothetical protein Y51A2B.6b - Caenorhabditis elegans
hypothetical protein Y51A2B.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T27067
R;McMurray, A.
Submitted to the EMBL Data Library, January 1998
A;Reference number: Z20305
A;Accession: T27067
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Typesmesters: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #Sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27684
R:Thomas, K.
Submitted to the EMBL Data Library, March 1996
                                                                                        Gaps
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A;Introns: 8/1; 33/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Yll6A8C.33
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                             Length 717,
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Pred. No. 1.7e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                        Indels
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                             DB 2;
50;
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A;Accession: T27684
A;Status: preliminary: translated from GB/EMBL/DDBJ
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Pred. No. 50;
1; Mismatches
                                                                                     1; Mismatches
                             68.6%; Score 35;
85.7%; Pred. No.
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66.7%;
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
                                                       Best Local Similarity 85.7
Matches 6; Conservative
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Matches 6; Conservative
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678 SFKPLPFER 686
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309 SFKPLPL 315
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309 SFKPLPL 315
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                                                                                                                                          2 SFKPMPL, 8
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C.Accession: G75378
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
M.; Shen, M., Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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A:Experimental source: strain R1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Deinococcus radiodurans
C.Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
   C;Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000
C;Accession: $56039; $64866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:91360365; PID:91360366; MIPS:YLR039C
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                                                                    Rivicuta, K.
submitted to the EMBL Data Library, December 1994
Streference number: $56039
A; Reference number: $56039
A; Reference number: $56039
A; Residues: DNA
A; Residues: 1-1056
A; Cross. references: EMBL: D43895; NID:g619062; PID:g633123
B; Koetter, P.; Rose, M.; Entian, K.D.
submitted to the Protein Sequence Database, May 1996
A; Reference number: $64863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Deinococcus radiodurans (strain R1)
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Pred. No. 1.2e+02;
1; Mismatches 1;
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C,Superfamily: Saccharomyces cerevisiae RIC1 protein
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2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                        A.Accession: $64866
A.Molecule type: DNA
A.Residues: 1-1056 <KOE>
A.Cross-references: EMBL: 273211; NII
A.Experimental source: strain $288C
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71.4%;
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75.0%;
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Best Local Similarity 71.4
Matches 5; Conservative
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Matches 6; Conserv
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91 YNFKPMAL, 98
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WNFKPMP 105
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A;Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66
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                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:273307; NID:g1360550; PIDN:CAA97706.1; PID:e245572; PID:g136055
A;Experimental source: strain S288C
C;Genetics:
submitted to the EMBL Data Library, June 1995
A:Description: 36.8 kb of S.cerevisiae chromosome XII including ACE2, CKII, PDC5, SLS1,
A:Reference number: S59313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Map position: 2
A:Introns: 151/1: 199/3: 277/1: 316/2: 352/3: 417/3: 449/1: 475/3: 577/1: 635/3: 728/3
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A:Cross-references: EMBL:254342; PIDN:CAA91156.1; GSPDB:GN00020; CESP:F26C11.1
A:Experimental source: clone C08H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Residues: i-755 <WI2>
A:Cross-references: EMBL:247072; PIDN:CAA87370.1; GSPDB:GN00020; CESP:F26C11.1
A:Experimental source: clone F26C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Species: Caenorhabditís elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T19118; T21390
R:Lloyd, C.
                                                                                                 A Accession: S59327
A Molecule type: DNA
A Residues: 1-748 A Molecule type: DNA
A Reference number: S64967
A Molecule type: DNA
A Molecule type: DNA
A Residues: 1-748 A Molecule type: DNA
A Molecule
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O.
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Pred. No. 82;
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A:Molecule type: DNA
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Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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$56039
RIC1 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein L1917; protein YLK039c
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBC Data Library, December 1994
A:Reference number: 219416
A:Accession: 721390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, October 1995
A: Reference number: 219074
A: Accession: T19118
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3; Mismatches
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62.5%;
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71.48;
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Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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703 YTFEPIPL 710
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P72845 synechocyst
P16788 human cytom
P38340 saccharomyc
P26205 trifolium r
P03076 mouse polyc
P53514 proteus mir
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erwinia her
salmonella
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escherichia
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drosophila
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saccharomyc
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                                               (without alignments)
4.677 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                             mycoplasma
                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                        February 27, 2002, 11:42:41; Search time 78.39 Seconds
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059448
P47694 r
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P27040
Q58597
P24010
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P76594
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P12349
P82094
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                  100059 seqs, 36664827 residues
                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                               SYT_METJA
COXI_BACSU
12C2_RAT
YFIQ_ECOLI
                                                                                                                                                                                                                                                                     PPAX_CAEEL
RIC1_YEAST
YAD8_SCHPO
SIR_SYNY3
GCVK_HCMVA
YB9H_YEAST
                                                                                                                                                                                                                                                                                                             BGLT_TRIRP
TAMI_POVM3
PMFC_PROMI
YES3_YEAST
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SY26_HUMAN
SODC_FRATU
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AVRB_MOUSE
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PER_DROVI
TMF1_HUMAN
SSD1_YEAST
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YMSS_CAEEL
TOP2_PEA
US20_HUMAN
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Maximum Match 100%
Listing first 45 summaries
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                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB scq length: 200000000
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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rhodobacter
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caenorhabdi
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                                                                                                  drosophila
                mycoplasma
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                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Matthews P., Lloyd C.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY; AN ORTHOPHOSPHORIC MONOESTER + H(2)0 • AN
ALCOHOL + ORTHOPHOSPHATE.
-!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                         067274
P45442
P47251
Q07982
P30052
P54246
P27997
P12978
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PROTON DONOR (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E7F3050115A235EB CRC64;
                                                                                                                                                                                                                                                                   PPAX_CAEEL STANDARD; PRT; 755 AA. 009549; Q17843; Q1.NOV-1995 (Rel. 32, Created) . 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annocation update) PUTATIVE ACID PHOSPHATASE F26C11.1 (EC 3.1.3.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred, No. 38;
1; Mismatches
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                                                                                                                                                                                                 AL IGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEAM; PF00328; acid_phosplat; 1,
PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, 247072; CAA87370.1; -.
EMBL, 254342; CAA87370.1; JOINED.
EMBL, 254342; CAA91156.1; -.
EMBL, 247072; CAA91156.1; JOINED.
WORMPEP, F26C11.1; CE05732.
InterPro; IPR000560; H15_acid_phosphtse.
Y4AS_RHISN
ATP_MCPN
ATP_EPROMO
TRMU_AQUAE
LAG2_CAEEL
SYS_MYCGE
GPO_ZYMMO
SCAL_DRCME
YNNZ_CAEEL
WNNZ_CAEEL
RBL1_RHOSH
EBN2_EBV
                                                                                                                                                         MHPA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Hydrolase.
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Best Local Similarity 71.4%;
Matches 5; Conservative
 181
239
339
402
417
4410
447
447
486
486
554
                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
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636
708
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636 6
702 7
755 AA;
 1 111:1
718 YQFKPLP 724
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 1 YSFKPMP 7
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SULFITE REDUCTASE (FERREDOXIN) (EC 1.8.7.1).
                                                                                                                                                                                                                                                                                                                                               635 AA.
                                                                                                                                                                                                                  Score 33; DB
Pred. No. 20;
                                                                                                                                                                                                                                          Mismatches
                                             or send an email to license@isb-sib.ch).
                                                                                                                                                 POTENTIAL.
                                                                                                                                                          POTENTIAL.
                                                                                                                                      POTENTIAL.
                                                                                                                                                                       POTENTIAL
                                                                              IPR001993; Mitoch_carrier.
                                                                                      Pfam; PF00153; mito_carr; 3,
PROSITE; PS00215; MITOCH_CARRIER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=8905231;
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75.08;
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Pfam; PF01077; NIR_SIR; 1.
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HSSP; P17846; 7GEP.
                                                                   EMBL; 256276; CAA91209.1; -
                                                                                                                           Transport.
                                                                                                                                                                                                                                         6; Conservative
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158.
190
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170 1
271 AA;
                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=97061201;
                                                                                                                                                                                                                                                                            1 YSFKPMPL 8
                                                                                                                                                                                                                                                                                                                                                                                                                SIR OR SLR0963.
                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                             SIR_SYNY3
P72854;
                                                                               InterPro;
                                                                                                                                     TRANSMEM
                                                                                                                                                           TRANSMEM
                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                    SIR_SYNY3
                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                 Koetter P., Rose M., Entian K.D.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE TRANSCRIPTION OF BOTH RIBOSOMAL PROTEIN
GENES AND RIBOSOMAL KNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi: Ascomycota: Saccharomycotina; Saccharomycetes:
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 1; Length 1056;
Pred. No. 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   1056 AA; 121649 MW; 2368616867AEAU31 CRC64;
                                                                                                                                                                                Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetales; Schizosaccharomycetaceae;
                                        01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTFEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                       PRT; 1056 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUTATIVE MITOCHONDRIAL CARRIER C4G8.08.
SPAC4G8.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; D43895; BAA07866.1; -. EMBL; 273211; CAA97567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.7
Best Local Similarity 75.0
Matches 6; Conservative
                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                           RIC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
NCB1_TaxID=4896;
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                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 YNFKPMAL 98
                                                                                                                                    NCBI_Tax.ID-4932;
                                                                                        RIC1 OR YLR039C.
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                                                                                                                                                                                                                                                                                                                                                                                          SCD; S0004029;
                                                                             PROTEIN
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Q09834;
                     RIC1_YEAST
P40395;
                                                                                                                                                                     Mizuta K
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RIC1_YEAST
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBUNIT: MONOMER (BY SIMILARITY).
-:- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA RES. 3:109-136(1996).

-!- CATALYTIC ACTIVITY: H(2)S + 3 OXIDIZED FERREDOXIN + 3 H(2)O
SULFITE + 3 REDUCED FERREDOXIN.

-!- COFACTOR: THIS BUXZME, CONTAINS ONE SIROHEME AND ONE 4FE-4S
IRON-SULFUR CENTER AS PROSTHETIC GROUPS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EF330C8CC8BDB6C4 CRC64;
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Bacteria: Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
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YB9H_YEAST
P38340;
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SEQUENCE
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BINDING
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Littler E., Stuart A.D., Chee M.S.;
"Human cytomegalovirus UL97 open reading frame encodes a protein that
phosphorylates the antiviral nucleoside analogue ganciclovir.";
Nature 358:160-162(1992).
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chee M.S., Bankler A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddle E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.: "Analysis of the protein-coding content of the sequence of human cytomegalovirus strain AD169.";
Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in human cytomegalovirus-infected cells.";
Nature 358:162-164(1992).
                                                    IRON SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) (POTENTIAL).
IRON-SULFUR (4FE-4S) AND SIROHEME (BY SIMILARITY).
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Sullivan V., Talarico C.L., Stanat S.C., Davis M., Coen D.M.,
                   5; NIR_SIR; 1.
Heme: Iron·sulfur; 4Fe-4S; Complete protecome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: PHOSPHORYLATES THE ANTIVIRAL NUCLEOSIDE ANALOG GANCICLOVIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sullivan V., Talarico C.L., Stanat S.C., Davis M., Coen D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sullivan V., Talarico C.L., Stanat S.C., Davis M., Coen D.M.
                                                                                                                                                                                                      Score 33; DB 1; Length 635;
Pred, No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SIMILARITY: BELONGS TO THE HCMV UL97 / HVS 36 FAMILY -:- SIMILARITY: TO TYROSINE-PROTEIN KINASES.
                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GANCICLOVIR KINASE (EC 2.7.1.-) (HSRF3 PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 34, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                             707 AA
                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cytomegalovirus (strain AD169).
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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MEDLINE-90269039; Pubmed-2161319;
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                                                                                                                                                                                                      64.78;
                                                                                                                                                635 AA; 71441
PR00397; STROHAEM
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Nature 366:756-756(1993)
                                                                       457
496
500
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                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                   1111:1 1
347 SFKPLPAWR 355
                     PS00365;
                                                                                                                                                                                                                                                                              2 SFKPMPLXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10360;
                 PROSITE; PS00365
Oxidoreductase;
                                                       451
457
496
500
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P1678B;
01-AUG-1990 (
01-AUG-1990 (
01-OCT-1996 (
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6
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                                                                                                                                                  SEQUENCE
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 PRINTS;
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GCVK_HCMVA
GCVK_HCMVA
CCVK_HCMVA
DT 01-AUG
DT 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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01-0cT-1994 (Rel. 30, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 26.1 KDA PROTEIN IN POP4-SHMI INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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ATP (BY SIMILARITY).
BY SIMILARITY.
74914183E5A5E03A CRC64;
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SEQUENCE 232 AA; 26068 MW; 66699F37B0013088 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                   PIR: S09862; OQBEJS.
HSSP: P06722: JAZO.
InterPro: JPR001245; TYL_kin.
PROSTTE: PS00107: PROTEIN_KINASE_ATP: 1.
PROSTTE: PS00107: PROTEIN_KINASE_TYR: 1.
PROSTTE: PS00119: PROTEIN_KINASE_TYR: 1.
TRANSE_TYR: PS00119: PROTEIN_KINASE_DOM: FALSE_NEG.
Transferase; Kinase: ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
55;
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-!- SIMILARITY: TO S.POMH: SPACL6E8.14C.
                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALA-RICH.
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MEDLINE=93220397; PubMed=8465606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78232 MW;
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55.6%;
                                                                                                                                                                                                                                             EMBL; X17403; CAA35333.1; -.
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PIR; S32963; S32963.
SGD; S0000465; YBR261C.
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456
407 AA;
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Best Local Similarity
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522 AFRPMPLQK 530
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Length 232;

DB 1;

Score 32;

62.78;

us-09-446-109a-4.rsp

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Proteus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF HYDROCYANIC ACID. WHICH FUNCTIONS AS A DEFENSE MECHANISM ACAINST SMALL PREDATORS, WHEN THE LEAF TISSUE IS DAMAGED.

-!- CATALITIC ACID. WHICH FUNCTIONS AS A DEFENSE MECHANISM ACAINST SMALL PREDATORS, WHEN THE LEAF TISSUE IS DAMAGED.

-!- CATALITIC SCATILITY: HYDROCYSIS OF TERMINAL, NON-REDUCING BETA-D-GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE.

-!- PATHAMY: CYANOGENESIS.

-!- SUBUNIT: HOMODIMER.

-!- SUBUNIT: HOMODIMER.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYI, HYDROLASES.
                                                                                                                                                                                                                                            Trifollum repens (Creeping white clover).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Pabales; Fabaceae; Papilionoideae: Trifolieae; Trifolium.
NCBL_TaxID=3899;
               Gaps
                                                                                                                                                                                                                                                                                                                                                                         Oxtoby E., Dunn M.A., Pancoro A., Hughes M.A.; Mulfectide and derived amino acid sequence of the cyanogenic betaglucosidase (linamarase) from white clover (Trifolium repens E.)."; plant Mol. Biol. 17:209-219(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
MEDLINE-96097401; Pubmed-8535788;
Barrett T., Suresh C.G., Tolley S.P., Dodson E.J., Hughes M.A.;
"The crystal structure of a cyanogenic beta-glucosidase from white clover, a family 1 glycosyl hydrolase.";
Structure 3:951-960(1995).
                                                                                                                                                             01-MAY-1992.(Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CYANOCENIC BETA-GLUCOSIDASE PRECURSOR (EC 3.2.1.21) (LINAMARASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC, ...) (POTENTIAL).
N-LINKED (GLCNAC, ...) (POTENTIAL).
20B983B65C47A678 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ptam: PF00232: Glyco_hydro_1; 1.—
PROSITE: PS00572: GLYCOSYL_HYDROL_FL_1; 1.
PROSITE: PS00653: GLYCOSYL_HYDROL_FL_2; 1.
Hydrolase: Glycosidase: Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYANOGENIC BETA-GLUCOSIDASE.
PROTON DONOR.
NUCLEOPHILE.
               Indels
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 12-25 AND 125-147.
STRAIN-S100 (EG); TISSUE-Leaf;
MEDLINE-91322517; Pubmed-1907511;
               1:
                                                                                                                                     425 AA
Pred. No. 27;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB; 1CBG; 15-OCT-95.
InterPro; IPR001360; Glyco_hydro_1.
                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X56733; CAA40057.1; -. PIR; S16580; GLJY14.
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213
220
412
425 AA;
                                                      1: 1111
225 YALKPMP 231
                                      1 YSFKPMP 7
                                                                                                                                                                                                                     (FRAGMENT).
                                                                                                                                   BGLT_TRIRP
P26205;
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DISULFID
CARBOHYD
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SIGNAL
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                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massad G., Mobley H.L.T.; "Genetic organization and complete sequence of the Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                    Mouse polyomavirus (strain 3).
Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Length 425;
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                                          Indels
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50831 MW; 63A8E82E532BCC37 CRC64;
  ı,
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
0UTER MEMBRANE USHER PROTEIN PMFC PRECURSOR.
                                                                                                                                                                                                                                                                              21.JUL-1986 (Rel. 01, Created)
21.JUL-1986 (Rel. 01, Last sequence update)
20.AUG-2001 (Rel. 40, Last annotation update)
Score 32; DB ]
Pred. No. 51;
4; Mismatches
                                                                                                                                                                                                                                        440 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          828 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A03613; TVVPM.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR003354; Papo_T_antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00226; DnaJ; 1.
Pfam; PF02380; Papo_T_antiqen; 1.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00636; DNAJ_1; FALSE_NEC.
PROSITE; PS50076; DNAJ_2; FALSE_NEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 8:855-860(1980).
-!- SIMILARITY: CONTAINS I J DOMAIN.
                                                                                                                                                                                                                                        PRT;
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62.7%;
50.0%;
                                          Conservative
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Best Local Similarity 50.0
Matches 5; Conservative
                                                                                                                                                                                                                                        STANDARD;
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Gene 150:101-104(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 YSYRALPIER 212
Query Match
Best Local Similarity
Matches 4; Consery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10635;
                                                                                                                                                                                                                                                                                                                                             MIDDLE T ANTIGEN
                                                                                                              ::|||:|:
10 HAFKPLPI 17
                                                                                     1 YSFKPMPL 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Early protein.
                                                                                                                                                                                                                                      TAMI_POVM3
P03076;
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EMBL; U18839; AAB64648.1; -. EMBL; U32508; AAB60298.1; -.
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Q02597;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potyvirus.
                                                                                                  TRANSMEM
                                                                                                                   TRANSMEM
                                                                                                                                             TRANSMEM
                                                                                                                                                            TRANSMEM
                                                                                                                                                                         SEQUENCE
                                                                                                                               TRANSMEM
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                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles, requires a license agreement (See http://www.isb-sib.ch/announce/or sendian email to license@isb-sib.ch).
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A. T., Carpenter J., Chen E., Cherry J.M. Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin.D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petell F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                            SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF PMF FIMBRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Korch C., Mountain H.A., Wenzlau J.M.;
Submitted (JUL-1995) to the EMBI/GenBank/DDBJ databases.
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                        OUTER MEMBRANE USHER PROTEIN PMFC.
                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INPOTHETICAL 164.4 KDA PROTEIN IN MET6-PUP3 INTERGENIC REGION.
                                        (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
                                                                                                                                                                                                                                         PROSTIE: PSO1151; FIRBRIAL_USHER: 1.
Outer membrane; Transmembrane; Fimbria; Transport; Signal.
SIGNAL 1 28 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                  62.7%; Score 32; DB 1; Length 828; 57.1%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                               0: Indels
                                                                                                                                                                                                                                                                                                       B11B05992A64BA44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1430 AA.
                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
             SUBUNITS ACROSS THE OUTER MEMBRANE.
                                                                                                                                                                                                   EMBL; 235428; CAA84590.1; -. InterPro; IPR000015; Fimb_usher. Pfam; PF00577; Usher; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: TO S.POMBE STE16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 967-1430 FROM N.A.
                                                                                                                                                                                                                                                                                                       93108 MW;
                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                        CHAIN 29
SEQUENCE 828 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       228 YAYKPLP 234
                                                                                                                                                                                                                                                                                                                                                                                                          1 YSFKPMP 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288C;
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P40061;
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YES3_YEAST
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01-JUL.1993 (Rel. 26, Created)
01-JUL.1994 (Rel. 29, Last sequence updatc)
01-JUN-1994 (Rel. 29, Last sequence updatc)
20-AUG-2001 (Rel. 40, Last amnotation update)
CENDROME POLYPROTEIN (CONTAINS IN TERMINAL PROTEIN (P1); HELPER
COMPONENT PROTEINASE (EC 3.4.22.-) (HC-PRO); PROTEIN P3; 6 KDA PROTEIN
1 (KL); CYTOPLASHIC INCLUSION PROTEIN (C1); 6 KDA PROTEIN 2
CENOME-LINKED PROTEIN (VPG); NUCLEAR INCLUSION PROTEIN A (NIA)
(EC 3.4.22.44) (49 KDA PROTEINASE) (49 KDA-PRO); NUCLEAR INCLUSION
PROTEIN B (NI-B) (NIB) (KNA-DIRECTED RNA POLYMERASE) (EC 2.7.7.48);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete nucleotide sequence of turnip mosaic potyvirus RNA."; J. Gen. Virol. 73:2785-2793(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the capsid protein gene.";
J. Gen. Virol. 712/69-2772(1990).
-!- FUNCTION: CYTOPLASMIC INCLUSION PROTEIN HAS HELICASE ACTIVITY.
MAY BE INVOLVED IN REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tremblay M.F., Nicolas O., Sinha R., Lazure C., Laliherte J.F.; "Sequence of the 3'-terminal region of turnip mosaic virus RNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6
                                                                                                                                                                                                                                                                                               Score 32; DB 1; Length 1430;
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                               07BB5D75BA204E50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1534-3163 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Turnip mosaic virus (strain Quebec) (TuMV).
                                                                                                                                                                                                                                                                                                                                            2; Mismatches
                                                                                          POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                            POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                            POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93057350; Pubmed=1431807;
Nicolas O., Laliberte J.F.;
SGD; S0000895; YER093C.
InterPro; IPR000651; RasGEFN.
Pfam; PF00618; RasGEFN: 1.
                                                                                                                                                                                                                                                                                               62.78;
71.48;
                                                                                                                                                                                                                                 164367
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity /1...
S; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                       400
585
640
890
1169
                                                                    Hypothetical protein;
                                                                                                                                                                                                                               1430 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_Tax1D=36396;
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600 HSFKPIP 606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase: Transferase; Thiol protease; RNA-directed RNA polymerase; Coat protein; Polyprotein; Covalent protein-RNA linkage; Helicase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 40, Last annotation update)
SMALL INDUCIBLE CYTOKINE ASE PRECURSOK (EOTAXIN-3) (MACKOPHAGE INFLAMMATOKY PROTEIN 4-ALPHA) (MIP-4-ALPHA) (CCL26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COVALENT LINKAGE OF VIRAL RNA (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.7%; Score 32; DB 1; Length 3163; 85.7%; Pred. No. 4.2e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 KDA PROTEIN 1.
CYTOPLASMIC INCLUSION PROTEIN.
6 KDA PROTEIN 2.
GENOME-LINKED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEAR INCLUSION PROTEIN A. NUCLEAR INCLUSION PROTEIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HELPER COMPONENT PROTEINASE. PROTEIN P3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL).
E -> G (IN REF. 2).
W, 6180F73B58DF6D59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-TERMINAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COAT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                   InterPro; IPR001730; Peptidase_C4.
InterPro; IPR001456; Peptidase_C6.
InterPro; IPR001540; Poty_P1.
InterPro; IPR001592; Poty_CP1.
InterPro; IPR001205; RNA_PO1_P3D.
InterPro; IPR001205; Trypsin.
Pfam; PF00863; Peptidase_C4; 1.
Pfam; PF00861; Peptidase_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00767; Poty_coat; 1.
Pfam; PF01577; Poty_P1; 1.
Pfam; PF00680; RNA_dep_RNA_pol; 1.
                                                                                                                                                                                                           InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00966; NIAPOTYPTASE.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICC; 1.
                                                                                                                        EMBL; D10927; BAA01725.1; -. EMBL; D10601; BAA01452.1; -. PIR; JQ1168; JQ1168. PIR; JQ2895; JQ1895.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2862 2862
3163 AA; 357817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3163
1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1320
                                                                                                                                                                                MEROPS; C04.001; -. MEROPS; C06.001; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2359
2876
1986
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Q9Y258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                              "A novel human CC chemokine, eotaxin-3, that is expressed in IL-4-stimulated vascular endothelial cells, exhibits potent activity toward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBCELLULAR LOCATION: SECRETED.
-:- TISSUB SPECIFICITY: UBIOLITOUSLY EXPRESSED AT LOW LEVELS'IN
VARIOUS TISSUBS INCLUDING HEART AND OVARY.
-:- SIMILARITY: BELONGS TO THE INTERCRINE BETA FAMILY (SMALL CYTOKINE
                                                                                  MEDLINE-99303563; PubMed-10373330;
Guo R.F., Ward P.A., Hu S.M., McDuffie J.E., Huber-Lang M., Shi M.M.;
"Molecular clouing and characterization of a novel human CC chemokine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning of a novel human CC chemokine (Eotaxin-3) that is functional ligand of CC chemokine receptor 3.".
J. Biol. Chem. 274.27975-27980 (1999)
J. Biol. Chem. 274.27975-27980 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                             Shinkai A., Yoshisue H., Koike M., Shoji E., Nakagawa S., Saito A.,
Takeda T., Imabeppu S., Kato Y., Hanai N., Anazawa H., Kuga T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitaura M., Suzuki N., Imai T., Takagi S., Suzuki R., Nakajima T.,
Hirai K., Nomiyama H., Yoshie O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Nomo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOKINE A26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; OB 1; Length 94; Pred. No. 16; 1; Indels 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Jones K., Graves T., Duckels G., Fronick W.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
BY SIMILARITY.
852581E4BDD39A5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00472; SMALL_CYTOKINES_CC: 1.
Cytokine: Chemotaxis: Inflammatory response: Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMALL INDUCIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001811; Chemokine_ILB.
InterPro; IPR000827; Small_cytokine_CC.
                                                                                                                                                                                                                         MEDLINE=99343775; Pubmed=10415065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99419089; PubMed-10488147;
                                                                                                                                                                                                                                                                                                                                                 Immunol. 163:1602-1610(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF124601; AAD22197.1; -. EMBL; AB016542; BAA36704.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC005102; AAD15411.1; -. EMBL; AB010447; BAA84579.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 AA; 10648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.88;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 71.4
استوری 5: Conservative
                                                                                                                                                       Genomics 58:313-317(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-C) (CHEMOKINE CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                 SEQUENCE FROM N.A.
              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB01044
MIM; 604697;
                                                                                                                                                                                                            TISSUE-Heart
                                                                                                                                                                                                                                                                                                                                  eosinophils.
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-4TCC 31510 / G-37;
MEDLINE-96026146; PubMed-7569993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Frischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchmann J.L., Weidmann J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
NGUYEN D.T., Utterback T.R., Sandck D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
The minimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
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Eukaryota: Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III; "A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HYPOTHETICAL 52,3 KDA PROTEIN IN HAP4-AAT1 INTERCENIC REGION.
                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 60.8%; Score 31; DB 1; Length 334; Similarity 57.1%; Pred. No. 63; 4; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 19 39 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F -> S (IN REF..2).
D142C358CE474C71 CRC64;
20-AUG-2001 (Rel. 40, Last annotation update) HYPOTHETICAL PROTEIN MG456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 175:7918-7930(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ATCC 33530 / G-37;
MEDLINE-94075230; Pubmed-8253680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94152173; PubMed-8109175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, 039727; AAC72476.1; -. EMBL, 039732; AAB01646.1; -. EMBL, U01730; AAD10612.1; -. TIGR; MC456; -.
                                                                                                                                                        Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 86-182 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDAR!,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
                                                                                             Mycoplasma genitalium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-S288C;
                                                                                                                                                                                 NCBI_TaxID=2097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 YNFEPLP 134
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P34252;
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                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision: Francisella group; Francisella.
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Pred. No. 34;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SUPEROXIDE DISMUTASE (CU-ZN) PRECURSOW (EC 1.15.1.1).
                                                                                                                                                                                 185 AA
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                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.8%;
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best Local Similarity 75.v
5.conservative
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                           Francisella tularensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-LVS;
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164 YSDKPQPL 171
   1 YSFKPMPI, 8
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Q59448;
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Gaps

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RESULT 14 Y456_MYCGE

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Cheret G., Pallier C., Valens M., Daignan-Fornier B., Fukuhara H., Bolotin-Fukuhara M., Sor F.;
"The DNA sequence analysis of the HAP4-LAP4 region on chromosome XI of Saccharomyces cerevisiae suggests the presence of a second aspartate aminotransferase gene in yeast.";
Veast 9:1259-1265(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.8%; Score 31; DB 1; Length 453; 66.7%; Pred. No. 86; 1. Indels 1. Indels
                                                                                                                                                                                                                                                                                                                                   EMBL; X71133; CAA81949.1; -.
EMBL; 228108; CAA81948.1; -.
PIR; S37935; S37935.
PIR; S39096; S39096.
SGD; S0001591; YKL108W.
Hypothetical protein.
SEQUENCE 453 AA; 52271 MW; 5282969C97AAEAC8 CRC64;
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Best Local Similarity 66.7
Matches 6; Conservative
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0

Gaps

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Search completed: February 27, 2002, 11:42:42 Job time: 541 sec

2 SFKPMPLXR 10 | | | | | | | 252 SFSPSPLIR 260

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February 27, 2002, 11:50:03 ; Search time 281.76 Seconds
(without alignments)
5.191 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                    473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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5: sp_invertebrate:*
6: Sp_mammal:*
7: sp_mhorate:*
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
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Sequence: '51
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1: sp_archea:*
2: sp_bacteria:*
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                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                      Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

092w19 arabidopsis P9503 mycobacteri 012098 saccharomyc 083066 fish lympho 0900v2 leishmanla 09v0v6 deinococcus 09ykhh human cytom 09yk16 human cytom 09yk9 human cytom 09yk9 human cytom 09yk9 human cytom 09yk18 laman cytom 09v18 caenorhabdi 06476 arabidopsis 016536 caenorhabdi 02345 arabidopsis 016536 caenorhabdi 02345 arabidopsis 016536 caenorhabdi 0959015 methanococc	09avp4 nicotiana t 091w81 arabidopsis 068101 human cytom 068102 human cytom 09ard0 lycopersico 09arc7 lycopersico
10 092W19 2 P95033 3 012098 3 012098 5 0900V2 5 0900V6 12 09YKG9 13 09YKG9 14 09YKG9 15 09YKG9 16 09YKG9 17 09YKG9 18 09YKG9 18 09YKG9 18 09YKG9 19 09YKG9 10 09YKG9 11 09YKG9 11 09YKG9 11 09YKG9 12 09YKG9 12 09YKG9 13 09YKG9 14 09YKG9 15 09YKG9 16 09YKG9 17 09YKG9 1	10 09LW81 10 09LW81 12 068101 12 068102 10 09ARD0 10 09ARC7 5 009238
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0108849988795555888888888888888888888888888	330 340 441 443 55

ALIGNMENTS

	370 AA.	se update)	annotation update)			Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Noodeoga: Endoatorumota: Diotera: Bruchumera: Muscomorpha:	Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; mustomorpha; Ephydroidea; Drosophilidae: Drosophila.				MEDLINE=20196006; Pubmed=10/31132; adams M.D. Celniker S.F. Holf R.A., Evans C.A., Godayne J.D.,	Amanatides P.G., Scherer S.E., I.I. P.W., Hoskins R.A., Galle R.F.,	shburner M., Henderson S.N.,	, Zhang Q., Chen L.X.,	G., Champe M., Preiffer B.D.,	Abril J.F., Aqbayani A., An HJ., Andrews-Pfannkoch C., Baldwin D.,	Ballew R.M., Bash A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	Borkova D., Borchan M.K., Bouck J., Blokstein F., Brocker F., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,	A.D., Dew I., Dietz S.M.,	., Ferriera S., Fleischmann W.,	Gelbart W.M., Glasser K.,	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N. I. Harvey D. Haiman T.T. Hernandey J.R., Houck J.,	Hostin D., Houston K.A., Howland T.J., Wei MH., Ibegwam C.,	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketonum K.A., Kimmal B.F. Kodira C.D. Kraff C., Kravitz S., Kulo D., Lai Z.,	Li Z., Liang Y., Lin X.,	•
	PRT; 37	Created) Last sequence update)	Last annota		it fly).	da: Trachea	rygota; bip Drosophila.	-			31132; jolf 8 A . F	LI P.W.	thards S., A	andell M.D.	, Blazej R.	HJ., Andr	lale J., Bay	man B.P., B	ler H., Cad	ke C., Dave	eng Z., Mays	., Ferraz C	Garg N.S.,	J.H., Gu Z.	aland T.J.,	G.H., Ke Z	N.A., Li J.,	
	PRELIMINARY;	(TrEMBLrel. 13, (TrEMBLrel. 13,	MBLrel.		Drosophila melanogaster (Fruit fly).	letazoa; Arthropo	Pterygota; Neoptera; Endopterygota; Dip Ephydroidea; Drosophilidae; Drosophila.	227;	M N.A.	SLEY;	MEDLINE-ZUL96006; PubMed-10/31132; Adams M.D. Celpiker S.F. Holf R	G., Scherer S.E	Lewis S.E., Ric	Worthan J.R., Y	, Rogers YH.C.	Aqbayani A., An	Basu A., Baxenc	Benos P.V., Ber	Busam D.A., But	Cawley S., Dahl	., Delcher A., De	Fvangelista C.C	Sabrielian A.E.,	Song F., Gorrell Harvey D. Hein	louston K.A., Hov	kodira C D Kr	ei Y., Levitsky /	
1 1 1	9W473 9W473;	2000	01-JUN-2001 (TrE	CG15767.	Drosophila m	Eukaryota; Me	Plerygota; N. Ephydroidea;	NCB1_Tax1D=7227;	SEQUENCE FROM N.A.	STRAIN-BERKELEY;	MEDLINE-ZOL9	Amanatides P	George R.A.,	Sutton G.G.,	Brandon R.C.	Abril J.F.	Ballew R.M.,	Beeson K.Y.,	Burtis K.C.,	Cherry J.M.,	de Pablos B.	Durbin K.J.,	Fosler C., G	Glodek A., G	Hostin D., H	Jalali M., K Kimmel B.F	Lasko P., Le	
RESULT	75 75 80 80	TO	DT	S	SO	႘႘	88	X C N	КР	۲ ک	X a	K Y	RA	ΚA	RA	A A	ΚA	RA:	R KA	RA	<u>×</u>	¥ ¥	RA	RA P	RA	KA V	¥ ¥	

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBL_TaxID=10116;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
3-HYDROXY-3-METHYLGLUTARYL COENZYME A REDUCTASE ISOFORM HMGRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 872;
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Pred. No 1.1e+02;
2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 protein.
872 AA; 92828 MW; 23CC61B4B296E948 CRC64;
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Last annotation update)
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Pred. No. 1e+02;
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
Allen P.B., Oulmet C.C., Greengard P.;
J. Blol. Chem. 0:0-0(1998).
EMBL; AF040954; AAB96775.1;
InterPro; IPR00571; Zf-CCCH.
InterPro; IPR003617; TFS2_N.
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-OCT-2000 (TrEMBLrel. 15, Last anno
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SMART; SM00356; ZnF_C3H1; 1.
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60.0%;
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Best Local Similarity 60.00,
"Thes 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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                                                                                                      Rattus norvegicus (Rat).
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01-JUL-1997 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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236 YNLKPIPLKR 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
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FB19.
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Sher E., Spradling A.C., Stapheton M., Skrong K., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Millens S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A C.J., Yeh R.-F., Zaveri J.S., Zhan M., Zhong G., Zhao Q., Zheng L.,
Chong X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
The genome, sequence of Drosophila melanogaster.",
Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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66.7%; Pred. No. 28;
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Bacteria: Cyanobacteria: Oscillatoriales: Trichodesmium.
NCBL_TaxID=104582;
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1784604660; AAF00916.1:
InterPro: JPR0006660; NIr_SIr.
Pfam: PF01077; NIR_SIR: 1.
PRINTS: PR00137; SIROHAEM.
PROSITE: PS001365; NIR_SIR: 1.
SEQUENCE 510 AA: 57584 MW; FJEDIBBEOBC8619F CRC64;
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PROSITE; PS50072; CSA_PPIASE_2; 1.
SEQUENCE 370 AA; 42460 MW; 388038EC1BA14F71 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Last sequence update)
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FERREDOXIN NITRITE REDUCTASE.
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O55000;
01-JUN-1998 (TrEMBLEEL: 06,
01-JUN-1998 (TrEMBLEEL: 06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.5
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2001 (TrEMBLrel. 17, Last annotation update)
01-UNAY-1001 (TrEMBLrel. 17, Last annotation update)
01-UNAY-1002 (TREMBLREL.)
01-METHYLTRANSFERASE I, 5-BISPHOSPHATE CARBOXYLASF/C***SENASE SMALL SUBUNIT
N-METHYLTRANSFERASE I.
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Eukaryota: Viridiplantae; Streptophyta: Embryop: ..: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: cor.: eudicots: Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta: Tracheophyta: Spermatophyta; Magnollophyta: eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Lin X., Kaul S., Town C.D., Benito M., Creasy T..., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bawman C.L., White O., Nierman W.C., Fraser C.M.;
Arabidopsis thaliana chromosome III BAC F17A17 genomic sequence.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EmbL; AFOSB900; AAC14296.1; -.
InterPro; IPR001214; SET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   504 AA; 57644 MW; B9CA9515863AAAAO CRC64;
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(TrEMBLrel. 17, Last annotation update)
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Pred. No. 92;
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Transferase; Methyltransferase.
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66.78;
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Matches 6; Conservative
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29 SFSPLPLSR 37
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                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots: Rosidae:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel.), Last annotation update)
B' REGULATORY SUBUNIT OF PP2A (ATB'ALPHA REGULATORY SUBUNIT OF PP2A).
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: UJ1525. AAB58900.1:
EMBL: AL162751: CAB83307.1:
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60.0%; Pred. No. 90;
iive 2; Mismatches 2
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Pred. No. 12;
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                                            Arabidopsis thaliana (Mouse-ear cress).
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MEDLINE-97274652; Pubmed-9128737;
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MEDLINE-96039620; Pubmed-7496400;
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Interpro, IPRO02554; B56.
Pfam; PF01603; B56; 1.
SEQUENCE 495 AA; 57536
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les 7; Conservative
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Matches 6; Conserv
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Pfam; PF00250; FOCK_head; I.
PRINTS; PR00053; FORKHEAD.
SMART; SM00339; FH; I.
PROSITE; PS00058; FORK_HEAD_2; I.
PROSITE; PS50039; FORK_HEAD_3; I.
SEQUENCE 510 AA; 55867 WW; 525
                                                                                STRAIN=N2;
MEDLINE=98013175; Pubmed=9353126;
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PRINTS; PR00053; FORKHEAD.
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Best Local Similarity 85.7%;
Matches 6; Conservative
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417 NFKPMPL 423
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Rhabditidae; Peloderinae; Caenorhabditis.
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MEDLINE-98013175; PubMed-9353126;
MEDLINE-98013175; PubMed-9353126;
DG9 S., Paradis S., Gottlieb S., Patterson G.I., Lee L.,
Tissenbaum H.A., Ruvkun G.;
"The Fork head transcription factor DAF-16 transduces insulin-like
metabolic and longevity signals in C. elegans.";
Nature 389:994-994(1997).
EMBL: AF020343; AAB84391.1;
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Transferase: Methyltransferase.
SEQUENCE 504 AA; 57613 MW; A5BB41F36FAB08BE CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FORK HEAD-RELATED TRANSCRIPTION FACTOR DAF-16A2.
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                                                               Score 35; DB
Pred. No. 92;
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MEDLINE-98028757; Pubmed-9360933;
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                                                  Query Match
Best Local Similarity 66.77
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Matches 6; Conservative
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Lin K., Dorman J.B., Rodan A., Kenyon C.; "daf-lis: An HNF-3/Gorkhead family member that can function to double the life-span of Caenorhabditis elegans."; Science 278:1319-1322(1997).
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NCBI_TaxID=6239;
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Tissenbaum H.A., Ruvkun G.;
The Fork head transcription factor DAF-16 transduces insulin-like metabolic and longevity signals in C. elegans.";
Nature 389:994-999(1997)
BEBL; AF02112; AAC47803.1;
FMBL; AF02312; AAB84390.1;
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Tissenbaum H.A., Ruvkun G.;
Tissenbaum H.A., Ruvkun G.;
The Fork head transcription factor DAF-16 transduces insulin-like metabolic and longevity signals in C. elegans.";
Nature 389:994-999(1997).
EMBI, AP20334; AAB84392.1;
TRANSFAC; T03400;
InterPro: IPR001766; Fork_head.
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1; Mismatches 0; Indels
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PROSITE; PS50039; FORK_HEAD_3; 1.
SEQUENCE 530 AA; 57898 MW; 8665FBDB428039D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52574F3F979B35B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
U-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FORK HEAD-RELATED TRANSCRIPTION FACTOR DAF-16B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530 AA.
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Nature 368:32-38(1994).
Caenorhabditis elegans
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                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-BRISTOL N2:

MEDLINE-94150718; Pubmed=7906398;

MIISON R., Ainscough R., Anderson K., Baynes C., Berks M.,

MILSON R., Ainscough R., Anderson K., Eaynes C., Berks M.,

A crarton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

A carton A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

A Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

A Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,

A parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

A smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,

Thomas K., Vaudin M., Vaughan K., Waterston R.,

Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

T. *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Jones K., Hinds K., Sutterer C., Cofman M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF039717; AAB96741.1; -.
HSSP: 063245; 2HFH.
Interpro: IPR001766; Fork_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00658; FORK_HEAD_2; 1.
PROSITE: PS50039; FORK_HEAD_3; 1.
SEQUENGE 622 AA; 69110 MW; 955771653C900E67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                         Created)
                                                                                                                              PRT;
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PRINTS; PR00053; FORKHEAD.
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01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2001 (TrEMBLrel. 17,
MIG2.7 PROTEIN.
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06,
17,
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Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                              PRELIMINARY;
                                                                                                                                                                     01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elegans.";
Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00339; FH;
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454 NEKPMPL 460
        :111111
437 NFKPMPL 443
                                                                                                                                                                                                                                   R13H8.1 PROTEIN.
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09x11c6;
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                                                                                        RESULT RE
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SEQUENTE FROM N.A.

SEQUENTE FROM N.A.

MEDLINE=54150718; PubMed=7906398;

WISON R., Alnscough K., Anderson K., Baynes C., Berks M.,

Bonfield J., Burron J., Connoll M., Copsey T., Cooper J., Cooper C.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

Jones M., Kershaw J., Kirsten J., Laister N., Lairelile P.,

Lightning J., Lloyd C., Mcmurrar A., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Kirken L., Roopra A., Saunders D., Shuwikeen R.,

Smaldon N., Smith A., Sonnhammer E., Staden R., Suliston J.,

Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston J.,

Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                    Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightching J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID-6239;
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85.7%; Pred. No. 1.38+02;
viemalches 0; Indels
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                                                                                                                                                                                                                                                                Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam: PF02206; WSN; 1.
SMART; SM00453; WSN; 1.
SEQUENCE 690 AA; 78360 MW; 0E8A2B2A2547F124 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 17, Last annotation update)
751A2B.6A PROFEIN.
751A2B.6A.
Caenorhabditis elegans.
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MEDLINE-94150718; Pubmed-7906398;
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Matches 6; Conservative
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EMBL: AL021493; CAA16394.1;

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MEDIENCE-94150718; PubMed-7906398;

MISON R., Ainscough R., Anderson K., Baynes C., Berks M.,

Milson R., Ainscough R., Connell M., Copsey T., Cooper J., Coulson A.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

Gardner A., Green P., Hawkins T., Hillier M., Latreille P.,

Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Rifken L., Roopra A., Sannders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhamer E., Staden R., Sulston J.,

Anterry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

Anterson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,

T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 045959 PRELIMINARY; PRT; 717 AA.
045959;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Y51A2B.6B PROTEIN.
Y51A2B.6B PROTEIN.
Cannorhabditis elegans.
Cannorhabditis elegans.
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TAXID-6239;
                                                                                                                                                                                                                                                                                                                                     0; Gaps
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Pred. No. 1.3e+02;
1; Mismatches 0; Indels
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Pred. No. 1.3e+02;
1; Mismatches 0; Indels
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                            EA9C79E40E7FBD6E CRC64;
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EMBL; AL021493; CAA16395.1: -.
InterPro: IPR03125; WSN.
Pfam; PF02206; WSN: 1.
SWART; SW00433; WSN: 1.
SEQUENCE 717 AA; 81489 MW; 1
                              InterPro; IPR03125; WSN.
PPfam; PR02206; WSN; 1.
SMART; SM00453; WSN: 1.
SEQUENCE 717 AA: 81475 MW;
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Best Local Similarity 85.7%;
Matches 6; Conservative
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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309 SFKPLPL 315
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Gaps .; 0

Search completed: February 27, 2002, 11:50:04 Job time: 983 sec

1111:11 309 SFKPLPL 315

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2 SFKPMPL 8

Sequence 11, Al Sequence 11, Al Sequence 15, Al Sequence 16, Al Sequence 45, Al Sequence 45, Al Sequence 6, Al Sequence 17, Al Sequence 17, Al Sequence 26, Al Sequence 27, Al

51

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database :

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GENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: Creminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSET: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTE: THM PC compatible OPERAT: M. SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
0.026;
                      PCT - US95 - 11126 - 11

US-08 - 299 - 285 - 15

US-08 - 299 - 285 - 15

US-08 - 299 - 285 - 15

US-08 - 295 - 125 - 15

US-08 - 295 - 285 - 15

US-08 - 299 - 285 - 17

US-08 - 299 - 285 - 17
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Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...p: US/08/299, 285
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"NET N° TREER: 63075

ACTION INFORMATION:

: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 7, Application US/08299285
; Patent No. 5696230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.4%;
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US-08-299-285-7
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TYPE: amino acid
STRANDEDNESS: not relev
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MOLECULE TYPE: peptide
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Best Local Similarity
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ZIP: 1310: 1
TELEPHOYER
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ATTORNEY
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\begin{smallmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} 
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Sequence 10, Appl
Sequence 24, Appl
Sequence 7, Appli
Sequence 10, Appli
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1.702 Million cell updates/sec
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                                                                                                                                                                                                                  Search time 132.19 Seconds
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6H_COMB.pep:*
/cgn2_6/ptodata/2/laa/FCUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/FCUS_COMB.pep:*
                                GenCore version 4.5
Copyright (c) 1993 · 2000 Compugen Ltd.
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US-08-299-285-24
US-08-985-126-7
US-08-985-126-10
US-08-985-126-24
PCT-US95-11126-7
US-08-299-285-5
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PCT-US95-11126-13
US-08-299-285-114
US-08-299-285-23
US-08-9985-126-14
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PCT-US95-11126-23
US-08-299-285-12
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PCT-US95-11126-12
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Score

Result . 9 ó 8

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APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Ainarsky, Leonid
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
                                                                                     TITLE OF INVENTION: High Affinity Response-Selective TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPL:CATION BATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPL:CATION DATA:
APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Jane E.
REGISTRATION NUMBER: 63075
TELECOMMUNICATION NUMBER: 63075
TELECOMMUNICATION NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-400
TELEFA: (215) 563-400
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
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1601 Market Street Suite 720
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                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                        Kirnarsky, Leonid
Taylor, Stephen M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESS: not relevant
not relevant
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TYPE: amino acid
STRANDEDNESS: not relev
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ZIP: 19103-2307
COMBUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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Best Local Similarity 80.0
Matches 8; Conservative
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                                                                      APPLICANT:
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                                                                                                                                                                                                                                                APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonin A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: Greminal Analogs of C5a Anaphylatoxin
WUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
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      Indels
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WEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG.1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Read, Janet E.
REGISTRATION NUMBER: 63075
TELEPHONE: (215) 563-404
INFORMATION POR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SECURIAL OF THE COMPUTER CANADATION:
TELEPHONE: (215) 563-404
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
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    Mismatches
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                                                                                                                                                                                       Sequence 10, Application US/08299285 Patent No. 5696230
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; Sequence 24, Application US/08299285
; Patent No. 5696230
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STRANDEDNESS: single
TOPOLOGY: not relevant
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Best Local Similarity 80.0
Local 8: Conservative
8; Conservative
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MEDIUM TYPE: Floppy
                                                               1 YSFKDMPLAR 10
                                         1 YSFKPMPLXR 10
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US-08-299-285-10
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Gaps

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APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Triarsky, Leoning
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C. Terminal Analogs of C5a Anaphylatoxin
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82.4%; Score 42; DB 2; Length 10;
80.0%; Pred. No. 0.026;
iive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALUNESSEE: Dann, Dorfman, Herrall and Skillman STREET: 1601 Market Street Suite 720 CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Parentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: "D-Alanine at position 9" US-08-985-126-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/985,126 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Reed, Janet E. REGISTARTION UNDBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. 5942599 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/08985126
Patent No. 5942599
GENERAL INFORMATION:
                                                                             REFERENCE/DOCKET NUMBER: 6307
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (215) 563-4100
FILING DATE: 31-AUG-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO FRAGMENT TYPF: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 80.0
Matches 8; Conservative
                                            NAME: Reed, Janet E. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YSFKPMPLXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-08-985-126-24
                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-985-126-10
Sequence 10, Application US/08985126
Patent No. 5942399
GENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2: Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
               ZIP: 19103-2307
COMPUTER REACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: Dann, Dorfman, Herrell and Skillman
F: 1601 Market Street Suite 720
Philadelphia
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APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 2;
Pred. No. 0.026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                      PILING DATE:
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION UNDER:
APPLICATION UNDER:
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTATION UNDERE: 36.752
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFHONE: (215) 563-4100
TELEFA: (215) 563-4044
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLLOGY: No. 5942599 Relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
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COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: NO. 59425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.4
Best Local Similarity 80.0
Matches 8; Conservative
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US-08-985-126-7
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STREET: 160
COUNTRY:
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APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Tinarsky, Leonid
APPLICANT: Traylor. Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : OTHER INFORMATION: /product= "D-Alanine at position 9" PCT-US95-11126-10
                                            Score 42; DB 5; tength 10;
Pred. No. 0.026;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 5; Length 10;
Pred. No. 0.026;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C.
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFCATION:
CLASSIFCATION:
PRIOR APPLICATION NUMBER: US 08/299,285
FILING DATE: 31.AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
RECISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4044
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
FENCTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                                                                                                                      FCT-US95-11126-10; Sequence 10, Application PC/TUS9511126; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC COMPATIBLE
                                              82.4%;
80.0%;
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80.0%;
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not relevant
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Best Local Similarity 80.0
Matches 8; Conservative
                                            Query Match 82.4
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: not re
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                                                                                                                                                       1 YSFKPMPLXR 10
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          82.4%; Score 42; DB 2; Length 10; 80.0%; Pred. No. 0.026; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C.
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PALENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                                                                                                    : LOCATTON: 9
OTHER*INEORMATION: "D-Alanine at position 9"
US-08-985-126-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
                 LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: No. 5942599 Relevant
TOPOLOGY: No. 5942599 Relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application PC/TUS9511126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 80.0
Matches 8; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                             1 YSFKPMPLXR 10
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PCT-US95-11126-7
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Gaps

us-09-446-109a-4.rai

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APPLICANT: Standerson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
WUMBER OF SQUIENCES: 37
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: High Affinity Response-Selective TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FLILIGE DATE: 31-AUG-1994
CLASSIFICATION: 530
                                                                                 ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.04;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-404
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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Matches 8; Conservative
                                                                                                                                                                                         ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                        NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YSFKPMPLXR 10
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                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                    Sequence 24, Application PC/TUS9511126
GENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Rinarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : OTHER INFORMATION: /product~ "D-Alanine at position 9" PCT-US95-11126-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42; DB 5; Length 10;
Pred. No. 0.026;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                           ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C.
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-299-285-5
Sequence 5, Application US/08299285
Patent No. 5696230
GENERAL INFORMATION:
APPLICANT: Sharman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
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TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                             STATE: PA
                                    PCT-US95-11126-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANT I - SENSE:
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APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCE: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        Length 10;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: US

ZOPPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-COS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Sulte 720
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                     Score 41; DB 2;
Pred. No. 0.04;
0; Mismatches
                                                                                                                       STRANDEDNESS: No. 5942599 Relevant TOPOLOGY: No. 5942599 Relevant
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TOPOLOGY: No. 5942599 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08985126; Patent No. 5942599; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 63075 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
    (215) 563-4100
                                                                                                                                                                                                                                                                                                                     80.4%;
80.0%;
                   TELEFAX: (215) 563-4044 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             ; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
US-08-985-126-5
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                                                                                        10 amino acids
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                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                   MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: NO
                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                          1 YSFKPMPLXR 10
                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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    TELEPHONE:
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APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
MUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.4%; Score 41; DB 1; Length 10; 80.0%; Pred. No. 0.04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: "D-Phenylalanine at OTHER INFORMATION: position 9" US-08-299-285-13
APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
CLASSIFICATION: 530
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APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                     REFERENCE, DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPAX: (215) 563-4100
TELEPAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE: CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5942599
GENERAL INFORMATION:
                                                           ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                  TOPOLOGY: not relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENET
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                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site LOCATION: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Bost Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                           TYPE: 'amino acid
STRANDEDNESS: not
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PCT-US95-11126-13
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                                                                                                                                                                     Gaps
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APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                               DB 2; Length 10;
                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C. STREET: 1601 Market Street Suite 720 CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACHONLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 5;
Pred. No. 0.04;
                                                                                                                               Score 41; DB 2;
Pred. No. 0.04;
0; Mismatches
: NAME/KEY: Modified-site
: LOCATION: 9
: OTHER INFORMATION: "D-Phenylalanine at
US-08-985-126-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FLLING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, JaneL E.
RECISTRATION NUMBER: 33,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             Sequence 5, Application PC/TUS9511126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
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                                                                                                                               80.4%;
80.0%;
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TELEFAX: (215) 563-4044
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-terminal
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                                                                                                                              Query Match 80.4
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                  1 YSEKPMPLXR 10
                                                                                                                                                                                                                       1 YSFKDMPLFR 10
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: FRAGMENT TYPE:
PCT-US95-11126-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                          PCT-US95-11126-5
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                                     APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUIENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                 ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C. STREET: 1601 Market Street Suite 720
CITY: Philodelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 9
COTHER INFORMATION: /product- D-Phenylalanine at
COTHER INFORMATION: position 9"
PCT-US95-111126-13
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 5;
Pred. No. 0.04;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTOKNEY/AGENT INFORMATION:
Sequence 13, Application PC/TUS9511126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36,252
ER: 63075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REPRENCE/DOCKET NUMBER: 6307
RELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFRAX: (215) 563-4104
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: C5a Anaphylatoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSS: not relevant not relevant
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YSFKPMPLXR 10
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                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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Search completed: February 27, 2002, 11:36:02 Job time: 141 sec

0

Gaps

0

0; Mismatches

1 YSFKPMPLXR 10

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80.4%; 80.0%;

Length 10; 2; Indels

400

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GenCore version 4.5
Copyright (c) 1993 · 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 27, 2002, 11:41:13 ; Search time 303.5 Seconds (without alignments) 5.125 Million cell updates/sec Run on:

US-09-446-109A-5

Title: Perfect score: Sequence:

1 RAARIŞLGPRXYSFKPMPLXR 21

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched: Total number of hits satisfying chosen parameters:

length: 0 length: 200000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

/SIDS8/gcgdata/geneseq/geneseqp/AA1980 /SIDS8/gcgdata/geneseq/geneseqp/AA1981. A_Geneseq_1101:* Database

/SIDS8/gcgdata/geneseq/geneseqp/AA1999_DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA2000_DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA2001_DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT. /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT. /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT: /SIDS8/gcgdata/geneseq/geneseqp/AA1989 DAT /SIDS8/gcgdata/geneseg/genesegp/AA1995.DAT /SIDS8/gcgdata/geneseq/geneseqp/AA1996.DAT /SIDS8/gcgdata/geneseq/genesegp/AA1998.DAT /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT /SIDS8/gcgdata/geneseq/geneseqp/AA1982.C /SIDS8/gcgdata/geneseq/geneseqp/AA1983.C /SIDS8/gcgdata/geneseq/geneseqp/AA1984.C /SIDS8/gcgdata/geneseq/geneseqp/AA1985.C /SIDS8/gcgdata/geneseq/geneseqp/AA1985.C /SIDS8/gcgdata/geneseq/geneseqp/AA1985.C /SIDS8/gcgdata/geneseq/geneseqp/AA1994

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Molecular adjuvant Molecular adjuvant Molecular adjuvant Molecular adjuvant Human complement Human complement Human complement Description AAW27251 AAW07785 AAW07786 AAW07786 AAW07787 AAW07789 AAW27254 AAW27256 10 % Query Match Length DB Score Result ş

Human compi. Human compieme. Human compiement c Human compiement c Human anaphylatoxi Human GSa protein Human CSa anaphyla	Numan C5a. Homo s Variant human C5a. Pro-C5 polypeptide Solid phase sequen Human C5a peptide C. pneumoniae prot C5a anaphylatoxin C5a anaphylatoxin C5a anaphylatoxin	Arabidopsis thalla Arabidopsis thalla Arabidopsis thalla C-terminal truncat C5a anaphylatoxin C5a anaphylatoxin Human secreted pro C-terminal truncat	CSa anaphylatoxin CSa anaphylatoxin CSa anaphyla L. intracellularis Mycobacterium tube H. pylori HPS117 p H. pylori HPC117 p Human protein sequ
AAW07783 AAW0783 AAW07804 AAW07791 AAW07792 AAW71666 AAR71666 AAR71666	AAB74053 AAB74119 AAR77604 AAW9580 AAB358 AAY3578 AAR94487 AAR94470 AAR94473	AAG27308 AAG27307 AAG27306 AAB74071 AAB94468 AAU01570 AAB74073	AAR94486 AAR94477 AAE05458 AAB52461 AAB52461 AAB46403 AAB464003
18 18 18 18 18 18 22	222 220 220 71 71	221 222 71 222 223	71 22 22 22 22 22 22
117 117 127 127 147	74 1676 1676 74 758 758 10	263 280 280 285 10 10 117 9	10 10 77 77 180 381 429 429
3 4 4 4 4 4 4 4 6 0 0 0 0 0 0 0 0 0 0 0 0	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	222-4-100	4 4 4 0 . 0 0 . 0 4 4 4 0 . 0 0 . 0 4 4 4 0 . 0 0 . 0 6 . 0 . 0 . 0 . 0 . 0 . 0 .
4 4 4 4 4 4 4 4 8 8 8 8 8 8 8 8 8 8 8 8		4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	40 40 40 40 40 40 40 39.5
12 13 14 15 16 17 19	2000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	22 33 33 34 34 34 35	38 39 44 44 44 55

ALIGNMENTS

/note= "Serum amyloid A is attached to the N-terminal" Molecular adjuvant; immune response; immunogen; binding affinity; antigen presenting cell; APC; viral pathogen; anti tumour response; antibody; immunodiagnostic; immunotherapeutic; agonist. /label= OTHER /wote= "Aminohexanoic acid which is a linear aliphatic spacer moiety" Location/Qualifiers AAW27254 standard; peptide; 12 AA. Molecular adjuvant formula 23-DEC-1997 (first entry) Modified-site Modified-site Synthetic AAW27254; Key AM27254 RESULT

Misc-difference 11 /note= "D-form residue" 96WO-US16825 18-OCT-1996; W09714426-A1 24-APR-1997

95US-0005727.

20-0CT-1995;

Human complement Human complement Human complement

Human complement

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WPI; 1997-244854/22
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                                                                                                                              response to an immunogen. The molecular adjuvant comprises a targeting response to an immunogen. The molecular adjuvant comprises a targeting response to an immunogen. The molecular adjuvant comprises a targeting ingand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ilgand being functionally linked to the immunogen, and so binding of the molecular adjuvant to the antigen presenting pathway of the molecular adjuvant to antigen presenting pathway of the APC. The present sequence represents a specifically claimed formula for a molecular adjuvant, where the immunogen is serum amyloid A. The molecular adjuvant can be used to produce an immune response for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiagnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and processed by APCs to provide APC mediated immune responses. It can provide for the production of antibodies against a weakly-antigenic or
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                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular adjuvant; immune response; immunogen; binding affinity;
                                                                Molecular adjuvants for enhancing immune responses - comprise an immunogen linked to a ligand having binding affinity for a determinant of an antigen presenting cell
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                                                                                                                                                                                                                                                                                                                                                              Score 51, DB 18; Length 12;
Pred. No. 0.054;
1; Mismatches 1; Indels
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                       Sanderson SD,
                                                                                                            Claim 15; Page 53; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW27250 standard; peptide; 10
                                                                                                                                                                                                                                                                                                                                                              51.0%;
83.3%;
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Best Local Similarity 83.3
Matches 10; Conservative
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 (UYNE-) UNIV NEBRASKA.
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response to an immunogen. The molecular adjuvant comprises a targeting response to an immunogen. The molecular adjuvant comprises a targeting response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ligand being functionally linked to the immunogen, and so binding of the molecular adjuvant to the APC determinant activates the APC, effecting delivery of the communogen to an antigen presenting pathway of the APC. The present sequence represents a specifically claimed targeting ligand, which is a C5a C-terminal decapeptide agonist. The molecular adjuvant can be used to to produce an immuno responses for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiagnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and immunotherapeutic agents. The molecular adjuvant is readily taken up and provide for the production of antibodies against a weakly-antigenic or non-antigenic substances.
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Molecular adjuvants for enhancing immune responses - comprise an immunogen linked to a ligand having binding affinity for a determinant of an antigen presenting cell
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Pred. No. 0.066;
0; Mismatches 1;
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                                                                                                                                                    Claim 5; Page 51; 61pp; English
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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Misc-difference
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response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ligand being functionally linked to the immunogen, and so binding of the molecular adjuvant to the APC determinant activates the APC, effecting delivery of the immunogen to an antigen presenting pathway of the APC. The present sequence, represents a targeting ligand and immunogen, in which the juxta-membrane epitope of imman mucin-1 is positioned toward the carboxyl terminus and the C5a analogue is positioned toward the amino terminus. The molecular adjuvant can be used to produce an immune
                                                                                                                                                                                                                                                response for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiagnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and processed by APCs to provide APC-mediated immune responses. It can provide
                                                                A novel molecular adjuvant has been developed for enhancing an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular adjuvant; immune response; immunogen; binding affinity; antigen presenting cell; APC; viral pathogen; anti tumour response; antibody; immunodiagnostic; immunotherapeutic; agonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18; Length 18;
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Pred. No. 0.12;
0; Mismatches
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determinant of an antigen presenting cell
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                                 Example 1; Page 31; 61pp; English
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90.0%;
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Best Local Similarity 90.0
9, Conservative
                                                                                                                                                                                                                                                                                                                                                        non-antigenic substances
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Misc-dlfference
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Gaps

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response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ligand being functionally linked to the immunogen, and so binding of the molecular adjuvant to immunogen to an antigen presenting personting pertenting of the molecular adjuvant to immunogen to an antigen presenting pathway of the APC, effecting delivery of the caquence represents a specifically claimed targeting ligand and immunogen. The molecular adjuvant can be used to produce an immune cresponse for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiagnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and processed controlled applyant is readily taken up and processed controlled to provide APC-mediated immune responses. It can provide to the production of antibodies against a weakly-antigenic or
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human complement C5a protein derivative analogue 1.
                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB 16
Pred. No. 0.13;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW07784 standard; protein; 64 AA.
Claim 6; Page 52; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                     50.08;
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                                                                                                                                                                                                                                                                                                                                                                     Query Match 50.0
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                      non-antigenic substances
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
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05-JUN-1995;
05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                       Seguence
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04-JUN-1996;
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                                                                                                                                                                                                       The present sequence, the human complement C5a derivative 1-64,
ThriMet, Cys27Ser, Asn64Cys, is a C5a receptor antagonist which
Exhibits no agonist activity. It can be used to treat or prevent
C5a mediated diseases or inflammation, e.g. pneumonitis, adult
respiratory distress syndrome (ARDS), pulmonary inflammation or
injury, post myccardial infarction inflammation inflammatory bost myccardial infarction inflammation or
disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
severe trauma and burns. It can also be used to treat patients
suffering from transplant rejection, receiving immunosuppressive
therapy or massive blood transfusion, exposed to medical devices
or experiencing pulmonary dysfunction following haemodialysis or
leukopheresis. It can also be used as a prophylactic, particularly
c in conditions caused by reperfusion following haemodialysis or
leukopheresis. It can also be used as a prophylactic, particularly
c inconditions caused by reperfusion, e.g. reperfusion following
ischemnia, and circulatory contact with medical devices, as well as
to prevent transplant rejection.
C Antibodies against the derivative can be used to detect or quantify
the derivative and modify, e.g. neutralise, its activity in vivo.
N.B. Sequence not given in specification, but constructed using the
wild type sequence given on pages 51-52.
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                                                                  New human complement C5a poly-peptide derivs. - used as C5a receptor antagonists, partic. for treating C5a-mediated diseases and inflammatory conditions
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Pred. No. 0.95;
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Misc-difference 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "wild type Ile replaced by Cys"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human complement C5a protein derivative analogue 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                   Example 3; Page -; 93pp; English
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Best Local Similarity 100.
Matches 10; Conservative
                    WPI; 1997-043125/04
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37 raarislgpr 46
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The present sequence, the human complement C5a derivative 1-65,
ThrlMeL, Cys27Ser, 11e65Cys, is a C5a receptor antagonist which
exhibits no agonist activity. It can be used to treat or prevant
C5a mediated diseases or inflammation, e.g. pneumonitis, adult
respiratory distress syndrome (ARDS), pulmonary inflammation or
injury, post myocardial infarction inflammation, inflammatory bowel
disease, rhemmatoid arthritis, psoriasis, endotoxic shock, sepsis,
severe trauma and burns. It can also be used to treat patients
suffering from transplant rejection, receiving immunosuppressive
therapy or massive blood transfusion, exposed to medical devices
or experiencing pulmonary dysfunction following haemodialysis or
leukopheresis: It can also be used as a prophylactic, particularly
in conditions caused by reperfusion, e.g. reperfusion following
ischaemia, and circulatory contact with medical devices, as well as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplant rejection. against the derivative can be used to delect or quantify {\bf q}
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                                                                                                                                                                                               Van Oostrum J;
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95US-0462648.
95US-0463224.
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                           Schmitz A, Van Heeke G,
                                                                                                                     (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                     WPI; 1997-043125/04
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                                          05-JUN-1995;
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Antibodies
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AAW07788
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                                                                                                                                                                                                                                                                         New human complement C5a poly-peptide derivs. - used as C5a receptor antagonists, partic. for treating C5a-mediated diseases and inflammatory conditions
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treatment; prevention; disease; inflammation; pneumonitis; burn;
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 /note= "wild type Thr replaced by Met" Misc-difference 27
                                 /note⇒ "wild type Cys replaced by Ser"
                                                          /note= "wild type Ser replaced by Cys'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human complement C5a protein derivative analogue 4.
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                                                                                                                                                     95US-0463377.
95US-0462648.
95US-0463224.
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Matches 10; Conservative
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                                             Misc-difference 66
Misc-difference 1
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Gaps
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 \cdot used as C5a receptor treating C5a-mediated diseases and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibodies against the derivative can be used to detect or quantify the derivative and modify, e.g. neutralise, its activity in vivo. N.B. Sequence not given in specification, but constructed using the wild type sequence given on pages 51-52.
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adult respiratory distress syndrome; ARDS; pulmonary; injury; post mycoardial; infarction; inflammatory bowel; endotoxic shock; rheumatoid arthritis; psoriasis; sepsis; transplant rejection; immunosuppressive therapy; blood transfusion; dystunction; haemodialysis; leukopheresis; prophylaxis; reperfusion.
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antagonists, partic. for
inflammatory conditions
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Best Local Similarity
Matches 10; Conserv
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AAW07788

Synthetic.

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Ouery Match
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Sequence

DB 18; Length 68;

Score 48;

48.0%;

100.08; 96WO-EP02422 (first entry) 10; Conservative Van Heeke G, antagonists, partic. for inflammatory conditions /note= GEIGY AG WPI; 1997-043125/04. Best Local Similarity 1 RAARISLGPR 10 37 raarisigpr 46 Misc-difference 69 Misc-difference 27 Misc-difference (CIBA) CIBA sapiens WO9639503-A1 04-JUN-1996; 05-JUN-1995; 05-JUN-1995; 05-JUN-1995; 01-SEP-1997 12-DEC-1996 Schmitz A, Synthetic AAW07789; 10 Matches AAW07789 New human complement C5a poly-peptide derivs. - used as C5a receptor antagonists, partic. for treating C5a-mediated diseases and inflammatory conditions the derivative and modify, e.g. neutralise, its activity in vivo. N.B. Sequence not given in specification, but constructed using the wild type sequence given on pages 51-52. Thirlibet, Cy273cr. Lys68Cys, is a Caracterion antagonist which exhibits no agonist activity. It can be used to treat or prevent C5a mediated diseases or inflammation, e.g. pneumonitis, adult respiratory distress syndrome (ARDS), pulmonary inflammation or injury, post myocardial infarction inflammation, inflammation bowel disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis, severe trauma and burns. It can also be used to treat patients suffering from transplant rejection, receiving immunosuppressive therapy or massive blood transfusion, exposed to medical devices or experiencing pulmonary dysfunction following haemodialysis or leukopheresis. It can also be used as a prophylactic, particularly in conditions caused by reperfusion, e.g. reperfusion following ischaemia, and circulatory contact with medical devices, as well as to prevent transplant rejection. Antibodies against the derivative can be used to detect or quantify Human: complement; C5a; derivative; receptor; antagonist; trauma; treatment; prevention; disease; inflammation; pneumonitis; burn; adult respiratory distress syndrome; ARDS; pulmonary; injury; post myocardial; infarction; inflammatory bowel; endotoxic shock; rheumatold arthritis; psoriasis; sepsis; transplant rejection; immunosuppressive therapy; blood transfusion; dysfunction; The present sequence, the human complement C5a derivative 1-68, hacmodialysis; leukopheresis; prophylaxis; repertusion /note= "wild type Cys replaced by Ser" /note- "wild type Lys replaced by Cys" /note= "wild type Thr replaced by Met" Human complement C5a protein derivative analogue 5. Van Oostrum J; Location/Qualifiers AAW07788 standard; protein; 68 AA Example 3; Page -; 93pp; English. 95US-0463377. 95US-0462648. 95US-0463224. 96WO-EP02422 (first entry) Schmitz A, Van Heeke G, (CIBA) CIBA GEIGY AG WPI; 1997-043125/04. Misc-difference Misc-difference Misc-difference Homo sapiens WO9639503-A1 04-JUN-1996; 05-JUN-1995; 05-JUN-1995; 01-SEP-1997 12-DEC-1996 05-JUN-1995

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Gaps
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                Indels
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Pred. No. 1;
Mismatches
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            Antibodies against the derivative can be used to detect or quantify the derivative and modify, e.g. neutralise, its activity in vivo. N.B. Sequence not given in specification, but constructed using the wild type sequence given on pages 51-52.
                                                                                                                                                                                                                                                                                                                                                                                                          Human: complement; CSa; derivative; receptor; antagonist; trauma; treatment; prevention; disease; inflammation; pneumonitis; burn; adult respiratory distress syndrome; ARDS; pulmonary; injury; post myocardial; infarction; inflammatory bowel; endotoxic shock; rheumatorid arthritis; psoriasis; sepsis; transplant rejection; immunosuppressive therapy; blood transfusion; dysfunction; haemodialysis; leukopheresis; prophylaxis; reperfusion.
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   transplant rejection.
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95US-0463224.
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Best Local Similarity 100.0°
Matches 10; Conservative
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37 raarislgpr 46
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                                                                                      69 AA;
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respiratory distress syndrome (ARDS), pulmonary inflammation or injury, post myocardial infarction inflammation or disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis, severe trauma and burns. It can also be used to treat patients suffering from transplant rejection, receiving immunosuppressive therapy or massive blood transfusion, exposed to medical devices or experiencing pulmonary dysfunction following hacmodialysis or leukopheresis. It can also be used as a prophylactic, particularly in conditions caused by reperfusion, e.g. reperfusion following ischaemia, and circulatory contact with medical devices, as well as to prevent transplant rejection.

Chatibodies against the derivative can be used to detect or quantify the derivative and modify, e.g. neutralise, its activity in vivo.

N.B. Sequence not given in specification, but constructed using the wild type sequence given on pages 51-52.
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100.0%;
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Matches 10; Conservative
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Gaps
New human complement C5a poly-peptide derivs. - used as C5a receptor antagonists, partic. for treating C5a-mediated diseases and inflammatory conditions
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Antibodies against the derivative can be used to detect or quantify the derivative and modify, e.g. neutralise, its activity in vivo.

W.B. Sequence not given in specification, but constructed using the wild type sequence given on pages 51-52.
                                                                                                                                                                                                    injury, post myocardial infarction inflammation, inflammatory bowel disease. Theumatoid arthritis, psoriasis, endotoxic shock, sepsis, severe trauma and burns. It can also be used to treat patients
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                                                                                                                               ThriGly, Cys27Ser, Gln7ICys, is a Csa receptor antagonist which exhibits no agonist activity. It can be used to treat or prevent C5a mediated diseases or inflammation, e.g. pneumonitis, adult respiratory distress syndrome (ARDS), pulmonary inflammation or
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1.1;
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100.0%; Pred. No. 1...
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                                                                           Claim 11; Page -; 93pp; English.
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RAARISIGPR 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difterence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9639503-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW07783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Gaps
                                                                                                                                                                                                                   receptor
                                                                                                                                                                                                                                                                                                                                        Thrighy, cys27Ser, His67Phe, Gla7ICys, is a C5a receptor antagonist which exhibits no agonist activity. It can be used to treat or agonist rectivity. It can be used to treat or adult respiratory distress syndrome (ARDS), pulmonary inflammation or injury, post myocardial infarction inflammation, inflammation or injury, post myocardial infarction inflammation, inflammatory bowel disease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis, severe trauma and burns. It can also be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prophylactic, particularly in conditions caused by reperfusion, e.g. reperfusion following ischaemia, and circulatory contact with medical devices, as well as to prevent transplant rejection. Antibodies against the derivative can be used to detect or quantify the derivative and modify, e.g. neutralise, its activity in vivo. N.B. Sequence not given in specification, but constructed using the wild type sequence given on pages 51-52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; complement; C5a; derivative; receptor; antagonist; trauma; treatment; prevention; disease; inflammation; pneumonitis; burn; adult respiratory distress syndrome; ARDS; pulmonary; injury; post myocardial; infarction; inflammatory bowel; endotoxic shock; rheumatoid arthritis; psoriasis; sepsis; transplant rejection; immunosuppressive therapy; blood transfusion; dysfunction; haemodialysis; leukopheresis; prophylaxis; reperfusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     patients suffering from transplant rejection, receiving immunosuppressive therapy or massive blood transfusion, exposed medical devices or experiencing pulmonary dysfunction following haemodialysis or leukopheresis. It can also be used as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                         present sequence, the human complement C5a derivative 1-71,
                                                                                                                                                                                                                 C5a
and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.0%; Score 48; DB 18; Length 71; 100.0%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                 poly-peptide derivs. - used as treating C5a-mediated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. nc.
                                                                                                                                           Van Oostrum J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human complement C5a protein derivative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW07804 standard; protein; 71 AA.
                                                                                                                                                                                                                                                                                       Claim 12; Page -; 93pp; English.
                                95US-0463377.
95US-0462648.
95US-0463224.
96WO-EP02422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-SEP-1997 (first entry)
                                                                                                                                                                                                               New human complement C5a antagonists, partic. for inflammatory conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 10: Conservative
                                                                                                                                           Schmitz A, Van Heeke G,
                                                                                                       (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                           WPI; 1997-043125/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RAARISLGPR 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Misc-difference 1
                                05-JUN-1995;
05-JUN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
04-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW07804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW07804
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Thribact. Cys27Ser, His67Phe, Gln71Cys, is a C5a receptor antagonist which exhibits no agonist activity. It can be used to treat or which exhibits no agonist activity. It can be used to treat or prevent C5a mediated diseases or inflammation. 4.9. pulmonary inflammation or injury, post myocardial infarction inflammation, inflammatory continury, post myocardial infarction inflammation, inflammatory continury, post myocardial infarction inflammation, inflammatory sepsis, severe trauma and burns. It can also be used to treat patients suffering from transplant rejection, receiving immunosuppressive therapy or massive blood transfusion, exposed to medical devices or experiencing pulmonary dysfunction following themediallysis or leukopheresis. It can also be used as a prophylactic, particularly in conditions caused by reperfusion, e.g. reperfusion following ischaemia, and circulatory contact with medical devices, as well as to prevent transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                  New human complement C5a poly-peptide derivs. - used as C5a receptor antagonists, partic, for treating C5a-mediated diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the derivative and modify, e.g. neutralise, its activity in vivo. N.B. Sequence not given in specification, but constructed using the wild type sequence given on pages 51-52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence, the human complement C5a derivative 1-71
        "wild type Thr replaced by Met"
                                                                           рy
                                           replaced
                                                                                                           "wild type Gln replaced
                                                                                                                                                                                                                                                                                                                                                 Van Oostrum J;
                                                                           "wild type His
                                        "wild type Cys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Page -; 93pp; English.
                                                                                                                                                                                                                                           95US-0463377.
95US-0462648.
95US-0463224.
                                                                                                                                                                                                             96WO-EP02422.
                                                                                                                                                                                                                                                                                                                                                 Schmitz A, Van Heeke G,
/note= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                    antagonists, partic. for inflammatory conditions
                                          /note=
                                                                           /note=
                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-043125/04.
                                                        Misc-difference 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA:
                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT47209
                      Misc-difference
                                                                                                                                                                                                             04 - JUN - 1996;
                                                                                                                                                                                                                                                               05-JUN-1995;
                                                                                                                                            WO9639503-A1
                                                                                                                                                                                                                                               05-JUN-1995;
                                                                                                                                                                            12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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DB 18; Length 71; Score 48; Pred. No. 48.0%; Scc. 100.0%; Pre Ouery Match Best Local Similarity Matches 10; Conservat

Conservative RAARISLGPR 10

raarislgpr 46

37

ò 8

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Gaps

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Indels

; 0

Mismatches

AAW07791 standard: protein; 71 AA AAW07791; RESULT 15 AAW07791

Human complement C5a protein derivative analogue 8.

(first entry)

01-SEP-1997

treatment; prevention; disease; inflammation; pneumonitis; burns adult respiratory distress syndrome; ARDS; pulmonary; injury; post myocardial; infarction; inflammatory bowel; endotoxic shock; rheumatorid arthritis; psoriasis; sepsis; transplant rejection; immunosuppressive therapy; blood transfusion; dysfunction; haemodialysis; leukopheresis; prophylaxis; reperfusion. Human; complement; C5a; derivative; receptor; antagonist; trauma /note= "wild type Cys replaced by ρλ /note= "wild type Thr replaced by /note- "wild type Gln replaced Location/Qualifiers Misc-difference 27 Misc-difference 1 Misc-difference Homo sapiens. Synthetic.

WO9639503-A1

12-DEC-1996

96WO-EP02422 04-JUN-1996;

95US-0463377. 95US-0462648. 05-JUN-1995; 05-JUN-1995; 05-JUN-1995;

(CIBA) CIBA GEIGY AG.

Van Oostrum J; o, Van Heeke Schmitz A,

WPI; 1997-043125/04.

New human complement C5a poly-peptide derivs. - used as C5a receptor aniagonists, partic. for treating C5a-mediated diseases and inflammatory conditions

Example 3; Page -; 93pp; English.

The present sequence, the human complement C5a derivative 1-71,
Thrimet, Cys27Ser, Gln71Cys, is a C5a receptor antagonist which
exhibits no agonist activity. It can be used to treat or prevent
C5a mediated diseases or inflammation, e.g. pneumonitis, adult
respiratory distress syndrome (ARDS), pulmonary inflammation or
injury, post myocardial infarction inflammation, inflammatory bowel
clisease, rheumatoid arthritis, psoriasis, endotoxic shock, sepsis,
severe trauma and burns. It can also be used to treat patients
suffering from transplant rejection, receiving immunosuppressive
therapy or massive blood transfusion, exposed to medical devices
contexperiencing pulmonary dystunction following hacmodialysis or
conditions caused by reperfusion following hacmodialysis or
conditions caused by reperfusion, e.g. reperfusion following
ischaemia, and circulatory contact with medical devices, as well as
to prevent transplant rejection.
Controles against the derivative can be used to detect or quantify
the derivative and modify, e.g. neutralise, its activity in vivo.
N.B. Sequence not given in specification, but constructed using the
wild type sequence given on pages 51-52.

71 AA; Sequence

Gaps . 0 DB 18; Length 71; Indels .; 0; Mismatches 48.0%; Score 48; 100.0%; Pred. No. Conservative Best Local Similarity Matches 10; Conserv Query Match Matches

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Search completed: February 27, 2002, 11:41:14 Job time: 453 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

February 27, 2002, 11:45:15 ; Search time 145.23 Seconds
(without alignments)
11.015 Million cell updates/sec

US-09-446-109A-5 100 1 RAARISLGPRXYSFKPMPLXR 21

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		٥				
		Query	•			
NO. S	Score	Match	Match Length	90	01	Description
1	48	48.0	1676	-	СЅНО	complement C5 prec
7	45	45.0	1195	~	B96746	probable kinesin T
m	42	42.0	118	~	S74769	hypothetical prote
4	42	42.0	495	7	T48372	AtB'alpha regulato
Ŋ	42	42.0	619	7	T24365	hypothetical prote
9	42	42.0	717	7	T27066	_
7	42	42.0	717	7	T27067	_
œ	41	41.0	069	7	T23775	hypothetical prote
6	41	41.0	881	-	A64040	hypothetical prote
10	41	41.0	921	7	T51136	ionotropic glutama
7	41	41.0	923	?	F84732	probable ligand-ga
12	40	40.0	381	7	C70711	hypothetical prote
13	40	40.0	429	7	E64617	hypothetical prote
14	40	40.0	733	7	E82525	primosomal protein
15	39	39.0	74	~	A01268	complement C5 - pi
16	39	39.0	308	~	C75073	hypothetical prote
17	39	39.0	457	7	503321	regulatory protein
18	39	39.0	208	٦	PWZMAM	H+-transporting AT
19	33	39.0	808	-	PWWTAM	H+-transporting AT
20	36	39.0	209	-	PWRZAM	H+-transporting AT
21	39	39.0	821	-	D65092	outer membrane ush
22	39	39.0	1011	7	C84524	probable disease r
23	38	38.0	74	7	A25408	complement C5 - bo
24	38	38.0	208	7	B70442	ribosomal protein
25	38	38.0	292	7	D86223	hypothetical prote
56	38	38.0	388		B41339	xylose isomerase (
27	38	38.0	388	7	JC1031	xylose isomerase (
28	38	38.0	389	-	ISSMXV	xylose isomerase (
29	38	38.0	394	-	ISSMXR	xylose isomerase (

A; Molecule type: mRNA A; Residues: 412-854, 'SLALSPRLECNGKISGHCKLRLPGSSDSPASASQVAGITGTHHHAQPT' <LUNNA A; Residues: 412-864, 19874 A; Cross-references: GB:K02874 A; Note: the carboxyl-terminal part of the sequence in this report appears to be delivened by Spanison, K.W.; Buko, A.M.; Ashworth, J.C.; Hill, H.R. Biochem J. 273, 635-640, 1991 A; Tille: Group B streptococci inactivate complement component C5a by enzymic cleavage A; Reference number: S15121; MUID:91144547

A: Molecule type: protein A: Molecule type: protein A: Relates: 678-751 (48-751 (48-751) (48-

A: Accession: A01267

A;Contents: annotation C;Contains two disulfide-linked chains, formed by removal of t (beta and alpha' chains).

C:Comment. Activation of C5 initiates the spontaneous assembly of the late complement is the foundation upon which the membrane attack complex is assembled. C:Comment: C5a has potent spasmogenic and chemotactic activity.

regulatory protein pisatin demethylas	cytochrome-c oxida	gene 43 procein - protein F1E22.10 (hypothetical prote	hypothetical prote	primosomal protein	primosomal protein	homeotic protein C	hypothetical prote	hypothetical prote	gly96 protein - mo	superoxide dismuta	differentiation-de	hypothetical prote
A28913 S45583	E69609	WZBE43 H96681	T52510	S59327	B86606	C72018	T30817	D72775	A72667	S33363	A33893	JC5537	A84727
1	7	7 7	7	7	7	7	7	7	7	7	٦	7	7
432	622	679 688	719	748	749	749	1426	134	140	153	154	156	192
38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	37.5	37.0	37.0	37.0	37.0	37.0
388	38	38 9 9 8	38	38	38	38	38	37.5	37	37	37	37	37
					_	_	_	_		۵.	_	_	

ALIGNMENTS

RESULT

CSHU
complement C5 precursor [validated] - human
N;Contains: C5a anaphylatoxin; C5b
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 08-Dec-2000
C; Accession: A40075; A27689; A01267; A01266; S15121
R; Haviland, D.L.; Haviland, J.C.; Fleischer, D.T.; Hunt, A.; Wetsel, R.A.
J. Emmunol. 146, 362-368, 1991
A; Title: Complete cDNA sequence of human complement pro-C5. Evidence of truncated tra
A; Reference number: A40075; MUID:91079575
A:Accession: A40075
A; Molecule type: mRNA
A; Residues: 1-1676 <hav></hav>
A;Cross-references: GB:MS7729; NID:g179982; PIDN:AAA51925.1; PID:g179983
A; Note: 518-Ser was also found
 R; Wetsel, R.A.; Lemons, R.S.; Le Beau, M.M.; Barnum, S.R.; Noack, D.; Tack, B.F.
Biochemistry 27, 1474-1482, 1988
A; Title: Molecular analysis of human complement component C5: localization of the str
A; Reference number: A27689; MUID:88209511
A; Accession: A27689
A; Molecule type: mRNA
A; Residues: 412-1676 < WFT>
A;Cross-references: GB:M65134; GB:M18879; NID:9179691; PIDN:AAA51856.1; PID:9179692
R;Fernandez, H.N.; Hugli, T.E.
J. Biol. Chem. 253, 6955-6964, 1978
A; Title: Primary structural analysis of the polypeptide portion of human C5a anaphyla
A;Reference number: A01267; MUID:79005687
3.3000000000000000000000000000000000000

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Gaps

;

Indels

5;

Length 118;

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S.
A:Reference number: S74322; MUID:97061201
A:Accession: S74769
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 < KMB.
A:Residues: 1-118 < KMB.
A:Residues: 1-118 < KMB.
A:Residues: 1-108 < KMB.
A:Residues: 1-108 < KMB.
Coss.references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAA16920.1; PID:g165
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: Synechocystis hypothetical protein slr1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AtB'alpha regulatory subunit of PP2A - Arabidopsis thaliana
N;Alternate names: protein F12E4.240
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T48372
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, March 2000
A;Reference number: 224492
A;Accession: T48372
A;Accession: T48372
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-495 <BEV>
A;Essidues: 1-495 <BEV>
A;Cross-references: EMBL:AL162751
A;Essidues: Source: cultivar Columbia; BAC clone F12E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A)Cross-references: EMBL:281581; PIDN:CAB04666.1; GSPDB:GN00019; CESP:T02E1.3b
A)Experimental source: clone T02E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T02E1.3b - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct.1999
C.Accession: T24365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Map position: 1
A:Introns: 17/3: 71/3; 102/3; 214/3; 255/1; 372/3; 398/1; 551/1; 634/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2; Length 495;
Pred. No. 17;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 2;
Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Richard, N. submitted to the EMBL Data Library, November 1996 A:Reference number: 219881 A:Accession: T24365 A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.0%; Score 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AARISLGPRXYSFKPMP 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 45.0
Matches 9; Conservative
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A; Residues: 1-679 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 5
A; Introns: 387/3
A; Note: F12E4.240
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                              A: Hope position: 9934.1-9934.1
C: Superfamily: alpha-2-macroglobulin
C: Superfamily: alpha-2-macroglobulin
C: Superfamily: alpha-2-macroglobulin
C: Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; if F: 1-18/Domain: signal sequence #status predicted <SIG>
F: 19-673,752-1676/Product: complement C5 #status predicted <C5B>
F: 19-673/Product: complement C5 #status predicted <C5B>
F: 19-673/Product: complement C5 alpha chain #status predicted <C5B>
F: 678-1676/Product: complement C5 alpha chain #status predicted <C5A>
F: 678-751/Product: C5B alpha' chain #status predicted <C5B>
F: 57-1676/Product: C5B alpha' chain #status predicted <C5B>
F: 58-1676/Product: C5B alpha' chain #status predicted <C5B>
F: 58-1676/Product: C5B alpha' chain #status predicted <C5B>
F: 57-1676/Product: C5B alpha' chain #status axperimental #status carbohydrate (Asn) (covalent) #status experimental
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R.Kaneko, T.: Sato, S.: Kotani, H.: Tanaka, A.: Asamizu, E.: Nakamura, Y.: Miyajima, N.: O. K.: Okumura, S.: Shimpo, S.: Takeuchi, C.: Wada, T.: Watanabe, A.: Yamada, M.: Yasuda DNA Res. 3, 109-136, 1996
A.Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cibate: Oz. Arabidopsis thaliana (mouse-ear cress)
Cispecles: Arabidopsis thaliana (mouse-ear cress)
Cispate: Oz.Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cispate: Oz.Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cispate: Oz. Mar. 2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
Cispate: Oz. Bispate: Oz. Cispate: Oz. Cispate: Oz. Mar. Conn. L.: Conway, A.B.: Conway, A.R.: Creasy, T.H.: Dewar, K.: Mar. N. C.: Hungles, B.: Huizar, L.
Naturnors: Hunter, J.L.: Jenkins, J.: Johnson-Hopson, C.: Khan, S.: Khaykin, E.: Kim, C.C. A.: Li, J.H.: Li, Y.: Lin, X.: Liu, Z.A.: Luros, J.S.: Maiti, R.: Marziali, Rizzo, M.: Rooney, T.: Rowery, D.: Sakano, H.
A.Authors: Salzberg, S.L.: Schwartz, J.R.: Shinn, P.: Southwick, A.M.: Sun, H.: Tallon, Ker, M.: Wu, D.: Yu, G.: Fraser, C.M.: Venter, J.C.: Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:751-752/Cléavage site: Arg-Leu (C5 convertase) #status experimental
F:911,1115,1630/Binding site: carbohydrate (Asn) (covalent) #status predicted
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hypothetical protein slr1068 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
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Pred. No. 13;
0; Mismatches
A;Cross-references: GDB:119734; OMIM:120900
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58.8%;
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Best Local Similarity 100.
Matches 10; Conservative
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Matches 10; Conservative
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A:Residues: 1-1195 <STO>
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A;Gene: T9N14.6
A;Map position: 1
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Length 679

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Length 690 8; Indels

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Richelschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage Gozayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Fiterence number: A64000; MUID:95350630
A:Accession: A64040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID:91574518; PIDN:AAC23317.1; PID:91574522
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R.Davenport, R.J.: Kiegle, E.A.: Tester, M.
submitted to the EMBL Data Library, December 1999
A.Description: G1R5, an ionotropic glutamate receptor ortholog from Arabidopsis.
A.Reference number: 225309
A.Accession: T51136
                                                                                                                                                                                                                                                                                      PIDN:CAB05258.1; GSPDB:GN00023; CESP:M162.7
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Haemophilus influenzae
C.bate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C;Accession: T23775
R;Basham, V.
Submitted to the EMBL Data Library, November 1996
A;Reference number: 219797
A;Reference number: 219797
A;Reference number: 219775
A;Retauts: prefluintary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-690 <WILL>
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A;Introns: 37/1; 389/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Y116A8C.33
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40.0%; Pred. No. 46;
tive 4; Mismatches 8; Indels
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A;Molecule type: mRNA
A;Residues: 1-921 <DAV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ilarity 47.4%; Score 41; DB. 47.4%; Pred. No. 35; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                         A)Cross-references: EMBL:282278; IA)Experimental source: clone M162
C)Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AARISLGPRXYSFKPMPLXR 21
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Best Local Similarity 40.07
Matches 8; Conservative
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Matches 9; Conserv
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Hypothetical, protein Y51A2B.6a - Caenorhabditis elegans

Hypothetical, protein Y51A2B.6a - Caenorhabditis elegans

C.Speciles: TYTOGE

R. R. McMurray, A.

R. Reference number: 220305

A. References: DNA

A. Residues: 1-717 (WIL)

A. Residues: 1-717 (WIL)

A. Residues: 1-717 (WIL)

A. Residues: LA References: EMBL: AL021493; PIDN: CAA16394.1; GSPDB: GN00023; CESP: Y51A2B.6a
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*Residucs: 1-717 cwtL.>
A;Cross-references: EMBL:AL021493; PIDN:CAA16395.1; GSPDB:GN00023; CESP:Y51A2B.6b
A;Experimental source: clone Y51A2B
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                                 Gaps
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A:Introns: 8/1; 33/1
C:Superfamily: Caenorhabditis elegans hypothetical protein Yll6A8C.33
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A;Introns: 8/1; 33/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Yll6ABC.33
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Pred. No. 25;
2; Mismatches
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   Pred. No. 23;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 47.4%;
Matches 9; Conservative
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41.28;
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                                                                                    3 ARISLGPRXYSFKPMPL 19
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Best Local Similarity 47.4 Matches 9; Conservative
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Best Local Similarity
Matches 7; Conserv
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A.Status: preliminary
A.Molecule type: DNA
A.Cross-references: GB.Ab004075; GB.Ab003849; NID:99107929; PIDN:AAF85486.1; GSPDB:GN
A.Stapson. A.J.G.; Reinach. F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
B.; Simpson. A.J.G.; Reinach. F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer
As-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Subuntited to GenBank, June 2000
A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
Chado, M.A.; Madeira, M.A.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Murtins
A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.; Marques, M.V.; Murtins
A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C. Go Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; de Oliveira, M.C.; Sawn,
A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva
A.Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                              Richard, J.E., White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.: Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe. Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
A; Akauthors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C.Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: 805525
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Scy
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Title: The complete genome sequence of the gastric pathogen Hellcobacter pylori. A;Reference number: A64520; MUID:97394467
A;Accession: E64617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: AE000590; GB: AE000511; NID: 92313907; PIDN: AAD07834.1; PID: 9231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA
A:Residues: 1-429 <TOM>
                                                                                                                                                                                                                                                      hypothetical protein HP0781 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primosomal protein N' XF2689 [imported] - Xylella fastidiosa (strain 9a5c)
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A;Note: for a complete list of authors see reference number A59328 below A;Accession: E82525
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Pred. No. 32;
2; Mismatches
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2; Mismatches
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50.08;
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Best Local Similarity 50.09
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                                                                                             63 ARVDLRERVVSFPPOPV 79
                                 3 ARISLGPRXYSFKPMPL
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                                                                                                                                                                                                                                                                                                                                                       C; Accession: E64617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable ligand-gated ion channel subunit [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species Atabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84732
R:Lin, X.; Kaul, S.; Ronnsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.A.; Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Roference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Rv1488 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Species: Mycobacterium tuberculosis
C:Date: 17-0ul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: C70711
R:Cole, S.T.: Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Raindream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, S37-544, 1998
A:Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A:Accession: C70711
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A:Experimental source: strain H37Rv
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A;Residues: 1-923 <STO>
A;Cross-references: GB:AE002093; NID:93831456; PIDN:AAC69938.1; GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.0%; Score 41; DB 2; Length 923 55.6%; Pred. No. 49;
                                                                                                                                                                                             Length 921
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Pred. No. 48;
                                                                                                                                                               41.0%; Scor.
55.6%; Pred. No. 40,
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A; Experimental source: cultivar Columbis C; Genetics:
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47.18;
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218 SIGERVYILHFGPDPLLR 235
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Best Local Similarity 55.67
Matches 10; Conservative
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Matches 8; Conservative
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Matches 10; Conservative
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A; Residues: 1-381 <COL>
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                                                                                         A; Map position: 2
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A: Map position: 2
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C;Superfamily:
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                                                        A;Gene: glr5
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3 ARISLGPRXYSFKPMP 18

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And 1288

And 1288

Complement C5 - pig (fragment)

N. Contains : C5a maphylatoxin. C5B

C. Species: Sus scrote domestica (domestic pig)

C. Species: Sus scrote domestica (domestic pig)

C. Species: Sus scrote domestica (domestic pig)

C. Accession: A01268; A26248

R. Gerard. C.: Hugh! T. S. A10-115, 1980

A; Title: Amino acid sequence of the anaphylatoxin from the fifth component of porcine or Accession: A01268; MUID: 80182137

A; Residues: 1-4 GERA

A; Residues: 1-7 GERA

R. Gerard. C.: Hugh! T. S. A. 78, 1833-1837, 1981

A; Residues: 1-7 GERA

R. Gerard. C.: Hugh! T. S. A. 78, 1833-1837, 1981

A; Residues: 1-7 A; Residues

A; Contents annotation; active region

A; Rooference number: A26247; MUID: 81199549

A; Contents: annotation; active region

A; Rooference number: A26248; MUID: 8184201

A; Residues: A56248; MUID: 8184201

A; Residues: A56248; MUID: 84184201

A; Residues: A56248; MUID: 84184201

A; Residues: 164, E; 66-73 ZIM-

C; Comment: Complement C5 contains two disulfide-linked chains, formed by removal of four (beta and alpha' chains)

C; Comment: Activation of C5 initiates the spontaneous assembly of the late complement cc comment: Activation of C5 initiates the spontaneous assembly of the late complement C; Comment: Activation of C5 initiates the spontaneous assembly of the late complement C; Comment: C5a has potent spasmogenic and chemotactic activity

C; Comment: C5a has potent spasmogenic and chemotactic activity

C; Comment: C5a has potent spasmogenic and chemotactic activity

C; Comment: C5a has potent spasmogenic and complement pathway; cytolysis; glycoprotein; I; F; 1-74/Product: C5a anaphylatoxin status experimental

F; 1-74/Product: C5a anaphylatoxin status experimental

F; 1-74/Product: C5a anaphylatoxin status experimental
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                                                                                                                                                                                                                                                                                                                                100059 seqs, 36664827 residues
GenCore version
Copyright (c) 1993 - 2000
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Q06735 beta vulgar	P22201 brassica na	P23413 raphanus sa	P05495 nicotiana p	P18260 helianthus	P16788 human cytom	Q10435 schizosacch	Q15155 homo sapien	P34434 caenorhabdi	Q64739 mus musculu	P13942 homo sapien	P20745 avian adeno
ATPO_BETVU	ATPO_BRANA	ATPO_RAPSA	ATPO_NICPL	ATPO_HELAN	GCVK_HCMVA	YDE1_SCHPO	PMSP_HUMAN	YL54_CAEEL	CA2B_MOUSE	CA2B_HUMAN	YOR3_ADEG1
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ALIGNMENTS

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"Molecular analysis of human complement component C5: Localization of the structural gene to chromosome 9."; Biochemistry 27:1474-1482(1988).
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Bohnsack J.F., Mollison K.M., Buko A.M., Ashworth J.C., Hill H.R.;

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"Primary structural analysis of the polypeptide portion of human C5a anaphylatoxin. Polypeptide sequence determination and assignment of the oligosaccharide attachment site in C5a.";
J. Biol. Chem. 253:6955-6964(1978).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 412-902 FROM N.A. MEDIJINE=81130937; PubMed=2579066; Lundwall A.B., Wetsel R.A., Kristensen T., Whitehead A.S., Woods D.E., Ogden R.C., Colten H.R., Tack B.F.; Isolation and sequence analysis of a cDNA clone encoding the fifth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-88309754; PubMed-3408713;
Zuiderweg E.R.P., Mollison K.W., Henkin J., Carter G.W.;
"Sequence-specific assignments in the 1H NMR spectrum of the human
                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wetsel R.A., Lemons R.S., Lebeau M.M., Barnum S.R., Noack D.,
                                                                 11-JUL-1986 (Rel. 01, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN).
1676 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement component.";
J. Biol. Chem. 260:2108-2112(1985)
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MEDLINE-79005687; PubMed-690134;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO C3, C4 AND ALPHA-2-MACROCLOBULIN.
SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 855
ONWARD DUE TO THE PRESENCE OF AN ALU REFEAT.
                                                                                                                                                                                 Heteronuclear three-dimensional NMR spectroscopy of the inflammatory
                                                     MEDLINE-89207527; PubMed-2784981; Zulderweg E.R.P., Nettesheim D.G., Mollison K.W., Carter G.W.; Zulderweg E.R.P., Nettesheim D.G., Mollison K.W., Carter G.W.; Tertlary Structure of human complement component C5a in solution from nuclear magnetic resonance data."; Biochemistry 28:172-185(1989).
                                                                                                                                                                                                                                                                                                                                         STRUCTURE BY NMR OF C5A.
MEDLINE-97732508. PubMed-188742:
Zhang X., Boyar W., Toth M.J., Wennogle L., Gonnella N.C.,
*Structural definition of the C5a C terminus by two-dimensional
                                                                                                                                                                                                                                       STRUCTURE BY NMR OF C5A.
MEDLINE=97160477; PubMed=9007977;
Zhang X., Boyar W., Galakatos N., Gonnella N.C.;
"Solution structure of a unique C5a semi-synthetic antagonist:
implications in receptor binding.";
Protein Sci. 6:65-72(1997).
                                                                                                                                                                                                                                                                                                                                                                                                 nuclear magnetic resonance spectroscopy.";
Proteins 28:261-267(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001599; Alpha_2_macroglobin.
InterPro; IPR00020; Anaphylatoxin.
InterPro; IPR001840; Anaphylatoxn.
                                                                                                                                         STRUCTURE BY NMR'OF C5A.
MEDLINE-89274164; Pubmed-2730871;
Zuiderweg. E.R.P., Fesik S.W.;
                                                                                                                                                                                             protein C5a.";
Blochemistry 28:2387-2391(1989),
 protein C5a.";
27:3568-3580(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001134; Netrin_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M57729; AAA51925.1; -. EMBL; M65134; AAA51856.1; -.
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                                           STRUCTURE BY NMR OF C5A
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1CFA; 17-SEP-97.
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PIR; S15121; S15121.
inflammatory
Blochemistry
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"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3466-3465(2001).
-!- CATALYTIC ACTIVITY: ANTHRANILATE + PHOSPHORIBOSYLPYROPHOSPHATE =
-!- PATLYTIC ACTIVITY: ANTHRANILATE + PROPHOSPHATE.
-!- FHOSPHORIBOSYL-ANTHRANILATE + PYROPHOSPHATE.
-!- SECOND STEP IN BIOSYNTHESIS OF TRYPTOPHAN.
-!- SIMILARITY: BELONGS TO THE ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE
-!- FAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                   Complement pathway; Complement alternate pathway; Glycoprotein; Plasma; Membrane attack complex; Cytolysis; Inflammatory response; Signal; Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision: Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                48.0%; Score 48; DB 1; Length 1676; 100.0%; Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                          COMPLEMENT C5 ALPHA CHAIN.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
                                                                    PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; FALSE_NEG PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
F -> S.
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MEDLINE=21145866; PubMed=11248100;
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                                        PRINTS; PR00004; ANAPHYLATOXN. SMART; SM0104; ANATO; 1.
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Pfam; PF01835; A2M_N; 1.
Pfam; PF01821; ANATO; 1.
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                            PF01759; NTR;
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P57856;
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STRAINED, KW20 / ATCC 51907;
MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams W.D., White O., Clayton R.A., Kirkness E.F.,
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gray C., Fountoulakis M.;
"Two-dimensional map of the proteome of Haemophilus influenzae.";
Electrophoresis 21:411-429(2000).
--- SIMILARITY: BELONGS TO THE PQIB FAMILY. STRONG, TO E.COLI YEBT.
                                                                                                                                                                                           .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
Gray C., Fountoulakis M.;
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole-genome random sequencing and assembly of Haemophilus
EMBL; AE006093; AAK02665.1; -.
InterPro: IPR003362; Anthr_phosphorbsyltransf.
InterPro: IPR000312; Glycos_transf_3.
InterPro: IPR000053; Thymid_phosphls.
ProDom; P000591; Glycos_transf_3; 1.
ProDom; P0005916; Thymid_phosphls.
ProDom; P0005916; Thymid_phosphls; 1.
Propom; P0005916; Thymid_phosphls; 1.
Tryptophan blosynthesis; Transferase; Glycosyltransferase; Complete proteome.
SEQUENCE 333 AA; 35880 MW; F42760CD105F6C5A CRC64;
                                                                                                                                                               Score 42; DB 1; Length 333;
Pred. No. 4.1;
                                                                                                                                                                                       5; Indels
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881 AA; 96677 MW; C278E5822E6A4F55 CRC64;
                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Complete proteome.
TRANSMEM 30 49 POTE
                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                              42.0%;
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245 RYTLTPQDFGFQPQPL 260
                                                                                                                                                                                           7; Conservative
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P44288;
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Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-HJRY;
MEDLINE-98295987; PubMed-9634230;
MEDLINE-98295987; PubMed-9634230;
Gotle S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.Y., Eiglumeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quil M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Suston J.E., Taylor K., Whitchead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.":
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole genome comparison of Mycobacterium tuberculosis clinical and
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41.0%; Score 41; DB 1; Length 881; 40.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laboratory strains.":
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE BAND 7 / MEC-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Transmembrane; Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUC-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 41.2 KDA PROTEIN RV1488.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                 381 AA.
                               Pred. No. 17;
; Mismatches
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Tubercuclist: Rv1488; -
TuterPro: IPR001107; Band 7
InterPro: IPR001972; Stomatin.
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                                                                   Conservative
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Query Match
Best Local Similarity
Matches 8; Conserva
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P71768;
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NCBI_TaxID=1061;
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MEDLINE=81199549; PubMed=6940191;
Gerard C., Hughl T.E.
Identification of classical anaphylatoxin as the des-Arg form of the C5a molecule: evidence of a modulator role for the oligosaccharide unit in human des Arg74-C5a.";
Proc. Natl. Acad. Sci. U.S.A. 78:1833-1837(1981).
                                                                                                                                                                 MEDLINE-80182137; PubMed-7372604; Gerard C., Hugli T.E.; "Amino acid sequence of the anaphylatoxin from the fifth component of
               Gaps
                                                                                                                               Eukaryota, Metázoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARE REQUIRED FOR 90% OF C5A ACTIVITY (ALTHOUGH ARG-74 IS NOT ESSENTIAL).
               ;
DB 1; Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement pathway; Complement alternate pathway; Plasma;
              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00104; ANATO; 1.
PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; PARTIAL.
PROSITE; PS01177; ANAPHYLATOXIN_1; 1.
PROSITE; PS01178; ANAPHYLATOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANAPHYLATOXIN-LIKE
                                                                                 74 AA.
              Mismatches
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InterPro: IPR000020; Anaphylatoxin.
InterPro: IPR001840; Anaphylatoxn.
Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 y response; 3D-structure.
21 47 ANAPHYLA:
22 54 34 55 ARE REQU
                                                                                                                                                                                              Biol. Chem. 255:4710-4715(1980)
                                                                           PRT;
                                                                                                                                                                                                                                                                        MEDLINE-90248365; PubMed-2337573;
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40.0%;
                           3 ARISLGPRXYSFKPMPL 19
                                   8; Conservative
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                                                                                                                                                                                        porcine complement.
Query Match
Best Local Similarity
                                                                                                                          scrofa (Pig).
                                                                                                                                                                                                                                                                  STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inflammatory
                                                           Matches
                                       q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SB1003;
MEDLINE-93360820; PubMed-8355615;
MEDLINE-93360820; PubMed-8355615;
MEDLINE-93360820; PubMed-8355615;
Sequence, genetic, and lacz fusion analyses of a nifr3-ntrB-ntrC operon in Rhodobacter capsulatus.";
MOL. Microbiol. 8:903-914(1993).
-: FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM NTRB/NTRC INVOLVED IN THE ACTIVATION OF NITROGEN ASSIMILATORY GENES SUCH AS GLNA. NTRC IS PHOSPHORYLATED BY NTRB AND INTERACTS WITH SIGMA-54.
-: SIMILARITY: THE N-PERMINAL REGION IS SIMILAR TO THAT OF OTHER REGULATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.
-: SIMILARITY: THE CENTRAL REGION CONTAINS A SIGMA-54 FACTOR INTERACTION ATP-BINDING DOMAIN.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones R., Haselkorn R.;
"The DNA sequence of the Rhodobacter capsulatus ntrA, ntrB and ntrC
gene analogues required for nitrogen fixation.";
Mol. Gen. Genet. 215:507-516(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                 Length 74;
                                                                                                                                                                                                                                                     1; Indels
                                                                                                                  11AAF2E94A026EB3 CRC64;
                                                                                                                                                                                              Score 39; DB 1;
Pred. No. 2.9;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P11028, 3F15.

InterPro; IPR001359; AAA.

InterPro; IPR00139; HSP0018-

InterPro; IPR001789; Response_reg.

InterPro; IPR02078; Sig54_interact.

Pfan; PF000178; sigma54; 1.

SMART; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=SB1003;
MEDLINE=89218961; Pubmed=2710108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NITROGEN REGULATION PROTEIN NTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTRC_RHOCA

ID NTRC_RHOCA STANDARD;

AC P09432;

DT 01-MAR-1989 (Rel. 10, Created)
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                                                                                                                                                                                              39.0%;
70.0%;
                                                                                                               8609 MW;
                                                                                                                                                                                              Query Match 39.0
Best Local Similarity 70.0
Matches 7; Conservative
26
40
62
64
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                                                                                                                                                                                                                                                                                                          1 RAARISLGPR 10
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
16
34
45
63
74 AA;
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us-09-446-109a-5.rsp

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InterPro; IPR000790; ATPase_A_C.
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                                                                                                                                                                                                                                                                                                       ATPO_MAIZE
P05494;
                                                                       ZN_FING
ZN_FING
ZN_FING
ZN_FING
SEQUENCE
         DOMAIN
ZN_FING
ZN_FING
ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                            RESULT 8
ATPO_MAIZE
                                                                                                                                                                                                                                                                                                                                                                                  ATPA.
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PROSITE: PS00675; SIGMA54_INTERACT_1: 1.
PROSITE: PS00676; SIGMA54_INTERACT_2: FALSE_NEG.
PROSITE: PS00688; SIGMA54_INTERACT_3: 1.
PROSITE: PS00688; SIGMA54_INTERACT_3: 1.
Nitrogen fixation: Transcription regulation: Repressor; Activator: DNA-binding: ATP-binding: Phosphorylation: Sensory transduction.
MOD_RES 53 53
PHOSPHORYLATION (BY SIMILARITY).
NP_BIND 171 178 ATP (POTENTIAL).
NP_BIND 171 178 ATP (POTENTIAL).
DNA_BIND 425 444 H-T-H MOTIF (BY SIMILARITY).
SEQUENCE 457 AA: 50042 MW; 7EB0484FE4740306 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Levin M.L., Chatterjee A., Pragliola A., Worley K.C., Wehnert M., Zhuchenko O., Smith R.F., Lee C.C., Herman G.E.;
"A comparative transcription map of the murine bare patches (Bpa) and Striated (Str) critical regions and human Xq28.";
Genome Res. 6:465-477(1996).
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART: SM00349; KRAB: 1.
SMART: SM0035; ZnF_CZH2; 9.
PROSITE: PS50805; ZnR_FRB: 1.
PROSITE: PS00028; ZNC_FINGER_CZH2_1: 8.
PROSITE: PS50157; ZINC_FINGER_CZH2_2: 9.
Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.
                                                                                                                                                                                                   ..
                                                                                                                                                                        39.0%; Score 39; DB 1; Length 457;
                                                                                                                                                                                                  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR
                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ZINC FINGER PROTEIN 92 (ZFP-92).
                                                                                                                                                                                                                                                                                                                 488 AA
                                                                                                                                                                                      Pred. No. 20;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 1 KRAB DOMAIN.
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Embryo;
MEDLINE-96425694; PubMed-8828036;
                                                                                                                                                                                                                                        303 RAERDGLGMRAFSAEAMGLVR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI 108094; Zfp92.
InterPro; IPR001909; KRAB.
InterPro; IPR000822; Znf-C2H2.
                                                                                                                                                                                                                         1 RAARISLGPRXYSFKPMPLXR 21
                                                                                                                                                                                    Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U47104; AAC52629.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01352; KRAB; 1.
Pfam; PF00096; zf-C2H2; 9.
                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                              2F92_MOUSE
062396;
                                                                                                                                                                       Query Match
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      SY TEFFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), CAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.
-i- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-i- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-88311189; PubMed-2900697;
Isaac P.G., Brennicke A., Dunbar S.M., Leaver C.J.;
The mitochondrial genome of fertile maize (Zea mays L.) contains two copies of the gene encoding the alpha-subunit of the FI-AFPase.";
Curr. Genet. 10:321-328(1985).
-: FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRADIENT ACROSS THE MEMBRANE, THE ALPHA CHAIN IS A REGULATORY
                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Braun C.J., Levings C.S. III;
"Nucleotide sequence of the F1-ATPase alpha subunit from maize
mitochondria ".
                                                                                                                                                                                                                                                                                                         1; Length 488;
                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1988 (Rel. 09, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL (EC 3.6.1.34).
                                                                                                                                                                                                                                6A649E30F2043699 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508 AA
                                                                                                                                                                                                                                                                                                            DB
ZINC FINGERS.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
                                                                                                                                                                                                                                                                                                      39.0%; Score 39; 42.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Physiol. 79:571-577(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                      432 C
55961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M16222; AAA70269.1; -. EMBL; 200026; CAA77319.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                         3 ARISLGPRXYSFKPMPLXR 21
                                                                                                                                                                                                                                                                                                    Query Match 39.0
Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
  432
163
191
219
247
275
303
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HSSP; P19483; 1COW.
                                                                                                                                                                                                                             488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays (Maize).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4577;
  141
141
169
197
225
253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion.
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30-MAY-2000
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9

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Gaps

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Indels

SO T T W X Y T T SO

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-I - SUBCELLULAR LOCATION: MITOCHONDRIAL.
-I - SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90016824; PubMed=2529479;
Schulte E., Staubach S., Laser B., Kueck U.;
"Wheat mitochondrial DNA: organization and sequences of the atpA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBJUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 17:7531-7531(1989).
-!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY
                                                                                                                           DB 1; Length 509;
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL (EC 3.6.1.34).
  ATP (BY SIMILARITY).
BY SIMILARITY.
7E6C7561B77C0668 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    509 AA
                                                                                                                                                                            8; Mismatches
                                                                                                                           Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000790; ATPase_A_C.
InterPro; IPR000194; ATPase_alpha_beta.
                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00422; ATP-synt_A-c; 1.
Pfam; PF00006; ATP-synt_ab; 1.
  178 A1
373 B1
55281 MW;
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                                                                                                                                                                                                                          1 RAARISLGPRXYSFKPMPLXR 21
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                                                                                                                           39.0%;
28.6%;
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28.6%;
                                                                                                                                                                                                                                                                        423 RGARLTEVPKOPOYEPLPIEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum (Wheat).
                                                                                                                                                     Local Similarity 28.6
es 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
  171
373
309 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P19483; 1COW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                       ATPO_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atp9 qenes."
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ACT_SITE
SEQUENCE
  NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                   RESULT 10
ATPO_WHEAT
                                                                                                                                                                                                                                                                                                                                                                                                                           P12862
                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                           F F 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(1), BETA(1), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A. B AND C. SUBCELLULAR LOCATION: MITOCHONDRIAL. SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT:
SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. JAPONICA; TISSUE=Shoot;
BEDLINE=29026808 P. Pubmed=2138730;
Kadowaki K.I., Boireau P., Laporte J.;
"Nucleotide sequence of the FI-Afpase alpha subunit gene from rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitochondria.";
Nucleic Acids Res. 18:1302-1302(1990).
-i- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
GRADIENT ACROSS THE MEMBRANE. THE ALPHA CHAIN IS A REGULATORY
                                                                                                                                                                                                                                                                                                                                                   .,
0
                                                                                                                                                                                                                                                                                39.0%; Score 39; DB 1; Length 508; 28.6%; Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                              7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL (EC 3.6.1.34).
                                                                                                                                                                       ATP (BY SIMILARITY).
BY SIMILARITY.
FBA3DD33141A0456 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probom; PD001099; ATPASE_A_C; 1.
PROSITE; PS00152; ATPASE_ALPHA_BETA; 1.
ATP Synthesis; CF(1); Hydrogen ion transport; Hydrolase; ATP-binding; Mitochondrion.
                                                                        Probom; Pb001099; Aréase_A_C; 1.
PROSITE; PS00152; ArASE_ALEHE_BETA; 1.
PTS synthesis; CF(1); Hydrogen ion transport;
Hydrolase; ArP-binding; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509 AA
                                                                                                                                                                                                                                                                                                                                                 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
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Interpro: IPR000194; ATPase_alpha_beta.
Pfam: PF0042; ATP-synt_A-C: 1.
Pfam: PF00006; ATP-synt_ab: 1.
IPR000194; ATPase_alpha_beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                       Pfam; PF00422; ATP-synt_A-c; 1. Pfam; PF00006; ATP-synt_ab; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                423 RGARLTEVPKOPOYEPLPIEK 443
                                                                                                                                                                                                                     508 AA; 55180 MW;
                                                                                                                                                                                                                                                                                                                                                                                               1 RAARISLGPRXYSFKPMPLXR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X51422; CAA35787.1; -. PIR; JQ0411; PWRZAM.
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                             Ouery Match:
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P19483; 1COW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP0_ORYSA
P15998;
                                                                                                                                                                                              ACT_SITE
SEQUENCE
                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTPO_ORYSA
ID ATPO_ORYSA
ID ATPO_ORYSA
OT 01-5988
DT 01-5988
DT 01-5988
DT 01-5988
DT 01-5988
DS 01/228
OS 01/228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 509;
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
2BD7893B255EF66B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                          Probom; PD001099; ATPase_A_C; 1.
PROSITE; PS00152; ATPASE_ALPHA_BETA: 1.
ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; ATP-binding; Mitochondrion.
Hydrolase; ATP-101011178 ATP (BY SIMILARI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39; DB ]
Pred. No. 22;
8; Mismatches
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õ a

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Zarbock J., Gendaro R., Romeo D., Clore G.M., Gronenborn A.M.;
"A proton nuclear magnetic resonance study of the conformation of bovine anaphylatoxin C5a in solution.";
FEBS Lett. 238:289-294(1988).
-!- FUNCTION: DERIVED FROW PROTECLYTIC DEGRADATION OF COMPLEMENT C5, C5 ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                       Gennaro R., Simonic T., Negri A., Mottola C., Secchi C., Ronchi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASOPHILIC LEUKOCYTES. C5A ALSO STIMULATES THE LOCOMOTION OF POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR MICHATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).

-!- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.

PIR; A25408; A25408.

INSS: PO1032; 1C5A.

InterPro; IPR001599; A1pha_2_macroglobin.

InterPro; IPR000202, Anaphylatoxin.
                                                                                                                                                                                                                                                               "C5a fragment of bovine complement. Purification, bloassays, amino-acid sequence and other structural studies."; Eur. J. Blochem. 155:77-86(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complement, pathway, Complement alternate pathway, Plasma;
Inflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38; DB 1; Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

CO9DF742D12D70F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PSO0477; ALPHA_2 MACROCLOBULIN; PARTIAL.
PROSITE; PSO1177; ANAPHYLATOXIN_1; 1.
PROSITE; PSO1178; ANAPHYLATOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANAPHY LATOX IN-LIKE
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20-AUG-2001 (Rel. 40, Last annotation update)
SOS RIBOSOMAL PROTEIN S5.
RPSE OR AQ_1645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Aquificales; Aquificaceae; Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 AA
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2; Mismatches
                                                                                                                                                                                                  MEDLINE-86136134; Pubmed-3081348;
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-89005703; PubMed-3262536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01821; ANATO; 1.
PRINTS; PR00004; ANAPHYLATOXN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.0%;
77.8%;
COMPLEMENT C5A ANAPHYLATOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8517 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00104; ANATO;
                                                                                                           Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 7: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RAARISLGP 9
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                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RS5_AQUAE
067563;
                                                                                                                                                                                                                                                                                                                                                             STRUCTURE
                                                                                                                                                                                                                                                 Romeo D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-K12 / MGIG55;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pram: PF00577; Usher: 1.
PROSITE; PS01151; FIMBRIAL_USHER: 1.
Hypothetical protein: Outer membrane; Transmembrane; Fimbria; Transport; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.0%; Score 39; DB 1; Length 821; 60.0%; Pred. No. 37;
                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001.(Rel. 40, Last annotation update)
HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN YQIG PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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(Rel. 12, Last sequence update)
(Rel. 33, Last annotation update)
                                                                                                                                                                             821 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 37;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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InterPro; IPR000015; Fimb_usher.
                                            423 RGARLTEVPKQPQYEPLPIEK 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000386; AAC76082.1; -.
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                1 RAARISLGPRXYSFKPMPLXR 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 60.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   Escherichia coli
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P12082;
01-OCT-1989 (
01-OCT-1989 (
                                                                                                                                                                      YQIG_ECOLI
P76655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
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ID COSA_BC
AC P12082;
DT 01-OCT
DT 01-OCT
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AC 01-NOS)
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                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                  -i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
PIR; S28986; S28986.
PDB: 1XXP: 31-MAY-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42792 MW; 99A941AA95920FCC CRC64;
CATALYTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.
COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 1;
Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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                                       - ! - SUBUNIT: HOMOTETRAMER.
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PDB; 1XYL; 31-MAY-94.
PDB; 1XYM; 31-MAY-94.
PDB; 2GYI; 10-JUL-95.
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                OF
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             MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Felman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                       Nature 392:353-358(1998).
-i- FUNCTION: PROTEIN S5 IS IMPORTANT IN THE ASSEMBLY AND FUNCTION THE 30S RIBOSOMAL SUBUNIT (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE S5P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS). MEDLINE-94215606; Pubmed-8180169; Lavie A., Allen K., Petsko G.A., Ringe D.; "X-ray crystallographic structures of D-xylose isomerase-substrate complexes position the substrate and provide evidence for metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
MEDLINE-89220983; PubMed-3508293;
Farber G.K., Petsko G.A., Ringe D.;
"The 3.0 A crystal structure of xylose isomerase from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmlcutes: Actinobacteria; Actinobacteridae;
Actinomycetales: Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-90057422; PubMed-2510821; Rarber G.K., Classfeld A., Tirraby G., Ringe D., Petsko G.A.; Crystallographic studies of the mechanism of xylose isomerase."; Biochemistry 28:7289-7297(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 1; Length 208;
Pred. No. 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Pram; PF00333; Ribosomal_S5; 1.
PROSITE; PS00585; RIBOSOMAL_S5; FALSE_NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 208 AA; 23211 MW; 06EDD421B17534C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          olivochromogenes.";
Protein Eng. 1:459-466(1987).
-:- FUNCTION: INVOLVED IN D-XYLOSE CATABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
XYLOSE ISOMERASE (EC 5.3.1.5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              movement during catalysis.";
Biochemistry 33:5469-5480(1994).
                                                                                                                                                                                                                                                                                                                                                                     3MBL; AE000749; AAC07536.1; -.
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41.2%;
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Matches 7; Conservative
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P15587;
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Pentose shunt; Xylose metabolism; Magnesium; 3D-structure.
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387 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

MEDLINE=89282788; PubMed=2734296;

AGarrell H.L., Glusker J.P., Burger V., Manfre F., Tritsch D.,

Biellmann J.-F.;

"X-ray analysis of D-xylose isomerase at 1.9 A: native enzyme in

"X-ray analysis of D-xylose isomerase at 1.9 A: native enzyme in

"X-ray analysis of D-xylose isomerase at 1.9 A: native enzyme in

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"Y-ray analysis of D-xylose isomerase at 1.9 A: native enzyme in

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                                                                                                                                                                                                                                                                                                                                      MEDLINE=92041569; PubMed=1657868; MeDLINE=92041569; PubMed=1657868; Mong H.C., Ting Y., Lin H.C., Reichert F., Myambo K., Watt K.W., Toy P.L., Drummond R.J.; Toy P.L., Drummond R.J.; Genetic organization and regulation of the xylose degradation genes in Streptomyces rubiginosus."; J. Bacteriol. 173:6849-6858(1991).
                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBL_TaxID=1929;
                                                                                                                                                          01-MAR-1992 (Rel. 21, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
XYLOSE ISOMERASE (EC 5.3.1.5).
                                                                                                                          387 AA
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PRINTS; PR00688; XYLOSISMRASE.
PROSITE; PS00172; XYLOSE_ISOMERASE_1; 1.
PROSITE; PS00173; XYLOSE_ISOMERASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB: 1XII: 22-UNN-94.
PDB: 1XII: 22-UNN-94.
PDB: 8XIA: 15-CT-91.
PDB: 9XIA: 15-UL-92.
InterPro: IPR001998; Xylose_isom.
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PIR; B41339; B41339;
PDB; 1XIS; 15-JUL-92.
PDB; 2XIS; 15-JUL-92.
PDB; 3XIS; 15-JUL-92.
PDB; 1XIS; 22-JUN-94.
PDB; 1XIC; 22-JUN-94.
PDB; 3XIC; 22-JUN-94.
PDB; 3XIC; 22-JUN-94.
PDB; 3XIC; 22-JUN-94.
PDB; 3XIC; 22-JUN-94.
                                                                                                                                                                                                                                                      Streptomyces rubiginosus.
                                                                                                                          STANDARD;
                    111 : 111
281 GPRHFDFKP 289
8 GPRXYSFKP 16
                                                                                                                      XYLA_STRRU
P24300;
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XYLA_STRRU
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8 GPRXYSFKP 16 ||| : ||| 281 GPRHFDFKP 289 o o

Search completed: February 27, 2002, 11:42:43 Job time: 542 sec

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February 27, 2002, 11:50:04 ; Search time 281.76 Seconds
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Sp. Vrus: *
Sp. Vertebrate: *
Sp. unclassified: *
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2: sp_bacteria:*
3: sp_tungi:*
4: sp_human:*
5: sp_lnvertebrate:*
6: sp_mammal:*
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sp_organelle:*
sp_phage:*
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Perfect score: 100
Sequence: 1 RAARISLGPRXYSFK
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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NO.	Score	Match	Match Length DB	DB	ID	Description
1	45	45.0	312	=	099LP8	nlnosnu smusenio
~	4.5	45.0	312	11	Q99LF3	0991f3 mus musculu
m	45	45.0	1195	10	Q9C7T0	09c7t0 arabidopsis
4	42.5	42.5	462	Ŋ	Q9GRM7	O9grm7 Leishmania
S	42	42.0	118	7	P72904	P72904 synechocyst
9	42	42.0	350	٣	000870	000870 fusarium so
7	42	42.0	495	10	004375	004375 arabidopsis
80	42	42.0	717	S	045958	045958 caenorhabdi
6	42	42.0	717	Ŋ	045959	045959 caenorhabdi
10	42	42.0	947	٣	Q9P449	09p449 schizophyll
11	42	42.0	1616	4	015054	015054 homo sapien
12	41	41.0	411	œ	Q9T719	09t719 lactoris fe
13	41	41.0	550	10	O9LLM4	Q911m4 eucalyptus
14	41	41.0	069	S	ogxuce	Q9xuc6 caenorhabdi
15	41	41.0	921	10	Q9SDQ4	09sdq4 arabidopsis
16	41	41.0	923	10	89.7260	092v68 arabidopsis
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18	40	40.0	266	7	007405	007405 mycobacteri
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05-76 09£76. 035470 helt. 034691 helianth. 090885 trypanosoma 090831 xylella fas 090838 homo sapien 090822 drosophila 038812 arabidopsis 090724 elymus sibi 090724 elymus sibi 090724 elymus sibi 090734 albulimima 091734 galbulimima 091734 jalbulimima 091731 pytococcus P7034 escherichia 091734 palbulimima 091735 cinnamodend 091767 nymphaea sp 091767 nymphaea sp 091776 cryptocarya 09m48 magnolia sp: 090761 piper bicol 091774 aristolochi	teleostomi; urinae; Mus. s.	e) a: Euteleostomi; ac: Murinae: Mus.
092GB8 091765 014691 014691 0908NS 0908NS 0909082 090902 0909034 090708 0907783 091783 0917750 0917750 0917750 0917750	ALIGNMENTS PRT; 312 AA. reated) ast sequence update ast annotation upda in. Craniata; Vertebra Sclurognathi; Muri 36448819FF529F7D Score 45; DB 11; Pred: No. 7.4;	PRT: 312 AA. PRT: 312 AA. 17, Created) 17, Last sequence update) PROTEIN MGC3262. data: Craniata: Vertebrata: mtia: Sciurognathi: Muridae;
40.0 40.0	Lrel. Lrel. Lrel. Lrel. Lrel. Chor ; Rodé ; Rodé ; Rodé 3490	PMPL]
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SEQUENCE FROM N.A. STRAIN=FRIEDLIN;
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                                                                                                                                                                                                                   Leishmania major.
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STRAIN=CV. COLUMBIA;

MEDINE-21016719; PubMed-11130712;

MEDINE-21016719; PubMed-11130712;

MITCHOLOGIS A. ECKET J.R., Palm C.J., Federspiel N.A., Kaul S.,

MITCHOLOGIS A., ECKET J. Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

MITCHOLOGIS A., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lucos J.S., Malti R., Marziall A.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Malti R., Marziall A.,

Millsscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta: Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Spermatophyta; Massicales; Brassicaces; Arabidopsis.
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                     Length 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP-binding; Coiled coil; MicroTubules; Motor protein. SEQUENCE 1195 AA; 133383 MW; 3DA8DF73184517F8 CRC64;
                                         Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC003289; AAH03289.1; -.
                                                                                                                312 AA; 34934 MW; 66EE82B3FF5FFF70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                Score 45; DB 11;
Pred. No. 7.4;
5; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1195 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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PRINTS; PR00380; KINESINHEAVY.
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InterPro; IPR001752; kinesin.
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                                                                                                                                                                                Ouery Match 45.0%;
Best Local Similarity 47.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                              268 ALLALGCKLYFFOPLPL 284
                                                                                                                                                                                                                                                                             3 ARTSLGPRXYSFKPMPL 19
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Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KINESIN, PUTATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                              SEQUENCE
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Q9C7T0
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                                                                                                                                                                                                         Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBL_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

BEDLINE-27061201;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Kimura T.,

Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,

Hisouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura

Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,

Tabata S.;
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Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A physical map of the Leishmania major Friedlin genome."; Genome Res. 8:135-145(1998).
EMBL; AL449144; AA-6744611.1; -
SEQUENCE 462 AA; 50128 MW; PF93BF8B907A7DD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.0%; Score 42; DB 2; Length 118;
41.2%; Pred. No. 8.7;
Live 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                       Saunders D., Murphy L., Harris D., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Complete proteome.
SEQUENCE 118 AA: 13731 MW; D384D5E6826D903C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyanobacteria; Chroococcales; Synechocystis
                                                                         Last sequence update)
Last annotation update)
KD PROTEIN.
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Last annotation update)
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  462 AA.
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01-FEB-1997 (TrEMBLrel. 02, Last seq
                                                   Created)
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PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=FRIEDLIN;
MEDLINE=98146435; PubMed=9477341;
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                                              01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, POSSIBLE HYPOTHETICAL 140.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.5%;
50.0%;
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Best Local Similarity 50.0°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3:109-136(1996).
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PRELIMINARY;
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Matches 7; Conserv
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2 AARISLGPRXYSFKPMP 18

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PRT;
    InterPro; IPR002554; B56.
Pfam; PF01603; B56; 1.
SEQUENCE 495 AA; 57536 MW;
                                                                                                       42.0%;
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                                                                                                                                                                                                               297 KVRRASLDKLANSFKPLPL 315
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InterPro; IPR003125; WSN.
Pfam; PF02206; WSN; 1.
SMART; SM00453; WSN; 1.
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                                                                                                       Ouery Match
Best Local Similarity 45.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 47.4
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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01-JUN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
Y51A2B.6B PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Arabidopsis thallana (Mouse-ear cress).

Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots; Rosidae; eurosids II; Brassicales: Brassicaceae: Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
B' RECULATORY SUBUNIT OF PP2A (ATB'ALPHA REGULATORY SUBUNIT OF PP2A).
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Lemcke K., Mayer K.F.X.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                Li D., Chung K.R., Smith D.A., Schardl C.L.;

"The Fusarium solani gene encoding kievitone hydratase, a secreted enzyme that catalyzes detoxification of a bean phytoalexin.";

MOI. Plant Microbe Interact. 8:388-397(1995).

EMBL; L39639; AAA87627.1; -...

SIGNAL 19
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MEDLINE-97274652: PubMed-9128737;
MEDLINE-97274652: PubMed-9128737;
MEDLINE-97274652: PubMed-9128737;
"Differential expression of three Arabidopsis genes encoding the regulatory subunit of protein phosphatase 2A.";
Eur. J. Biochem. 245:156-163(1997).
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                                                                                                                                                                                                                                                                                  Eukāryota; Fungl; Ascomycota; mitosporic Ascomycota; Fusarium.
NCBI_TaxID=108890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 350,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL: U715526: AAB58900.1;
EMBL: AL162751: CAB831307.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIEVITONE HYDRATASE.
CE09807A7B34C91B CRC64;
                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
KIEVITONE HYDRATASE PRECURSOR.
                                                                                                                      350 AA
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28;
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L; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42;
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MEDLINE-95383711; Pubmed-7655061;
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PRELIMINARY;
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350
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             Fusarium solani.
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X MEDLINE-94150718; PubMed-7906398;

Wilson R. Ainscough R., Anderson K., Baynes C., Berks M.,

Wilson R., Ainscough R., Conell M., Copsey T., Cooper J., Coulson A.,

Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,

A Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

A Gardner A., Green P., Hawkins T., Hiller L., Jahr M., Johnston L.,

A Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,

Smaldon N., Smith A., Sonnhamer E., Staden R., Sulston J.,

Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

A Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;

Elegans J.,

E
                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                              Length 495;
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                                                                                                                                                                                                                                                              Indels
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545F041C4ACB4A29 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     045958;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Y51A2B.6A.
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06, Last sequence update)
17, Last annotation update)
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47.4%; Pred. No. 61;
tive 2; Mismatches
                                                                                                                                                    Score 42; DB J
Pred. No. 41;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      717 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           717 AA.
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Caenorhabditis elegans.
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Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

DNA Res. 4:141-150(1997).
                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 4; Length 1616;
Pred. No. 1.5e+02;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B571D366792E8B9C CRC64;
                                              015054;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
KIAA0346 PROTEIN (FRAGMENT).
                                 1616 AA
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001440; TPR.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR003347; JmjC.
                                 PRT;
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                                                                                                                                                                                                                                                                        MEDLINE=97349984; PubMed=9205841;
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SEQUENCE 1616 AA; 174113 MW;
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                                PRELIMINARY;
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Best Local Similarity 58.37
Best Local 7; Conservative
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                                                                                                                                                     Homo sapiens (Human)
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015054
015054
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                                                                                                                                                              MEDLINE-94150718; PubMed-7906398; Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Benteld J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Carakton M.; Dear S., Du Z., Durbin R., Favello A., Fulton L., Jones A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thomas K., Vaudin M., Vaudhan R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; Therry-Mieg J., Thomas K., Wuldin M., Vaudhan F.; Baten B., Contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Stereales; Schizophyllaceae; Schizophyllum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=UVMT30;
Shen G., Chen Y., Song D., Peng Z., Novotny C.P., Ullrich R.C.;
Shen G., Chen Y., Song D., Peng Z., Novotny C.P., Ullrich R.C.;
The A-alpha6 mating-type locus of Schizophyllum commune.";
Submitted (Julv-200) to the EMBL/GenBank/DDBJ databases.
EMBL; AF274566; AAF78245.1;
FIREFFCTO: [FR001356; Homeobox.
SMART: SM00389; HOX. 102915 MW; 9CSDA6BEB661S9B7 CRC64;
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                                                                                                                  Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717 AA; 81489 MW; 14E394886B373AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNI-2001 (TrEMBLrel. 17, Last annotation update)
MATING TYPE PROTEIN A-ALPHA 26.
Schlzophyllum commune (Bracket fungus).
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Pred. No. 83;
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Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL021493; CAA16395.1; -.
InterPro; IPR003125; WSN.
Pfam; PF02206; WSN: 1.
SMART: SM00453; WSN: 1.
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Best Local Similarity 47.41
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
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                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                SEQUENCE FROM N.A.
                                                NCBI_TaxID=6239;
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SUBUNIT (EYSIMILARITY).

SUBUNIT: F-TYPE ATPASSE HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBUNITS: ALPHA(3), BETA(3), GAMA(1), DELTA(1), EPSILON(1).

HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).

- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE (BY
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20052162; PubMed=10586879; Olu Y.L., Lee J., Bernasconl'Quadroni F., Soltis D.E., Soltis P.S., Zanis M., Zimmer E.A., Chen Z., Savolainen V., Chase M.W.; "The earliest angiosperms: evidence from mitochondrial, plastid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cuxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Piperales; Lactoridaceae; Lactoris.
NCBI_TaxID+22303;
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                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ATPASE ALPHA SUBUNIT (FRAGMENT).
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RESULT

Matches

ô 9

TO ATP SYNTHASE ALPHA CHAIN, C TERMINUS.

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

qq ò

Basham V.;

Search completed: February 27, 2002, 11:50:06

Wilson R., Ainscould R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Farello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Menurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mo Contiguous nucleotide sequence from chromosome III of C. Address 38, 32-38 (1994).

BMBL; 282278; CAB05258.1; -.

EMBL; PFO2 IPRO31125; WSN.

Pfam; PF02206; WSN: 1.

SMART; SM00453; WSN: 1.

SEQUENCE 690 AA; 78360 MW; 0E8A2B2A2547F124 CRC64; SEQUENCE FROM N.A. MEDLINE-94150718; PubMed-7906398; Pfam; PF00060; Lig_chan; 1. Pfam; PF01094; ANF_receptor; 1. SMART; SM00079; PBPe; 1. 311 KVKRASLDNLASSFKPLPL 329 1 RAARISLGPRXYSFKPMPL 19 6 SLGPRXY -- SFKPMPLXR 21 Overy Match
Best Local Similarity 47...
Best Local Similarity 47...
Gonservative 10; Conservative PRELIMINARY; Best Local Similarity Matches 10; Conserv [1] SEQUENCE FROM N.A. NCBI_TaxID=3702; Query Match 09SD04; **09SD04** RESULT 15 GLR5. 09SD04 ò ; Pfam: PF00422; ATP-synt_A-c; 1.
Pfam: PF0006; ATP-synt_ab: 1.
ProDom: PD001099; ATPase_A-c; 1.
ATP Synthesis; ATP-binding; CF(1); Hydrogen ion transport; Hydrolase; Eucalyptus camaldulensis (Murray red gum).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Myrtales; Myrtaceae; Eucalyptus.

NCBI_TaxID=34316; Gaps Gaps Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. ; 0 . 0 Score 41; DB 10; Length 550; Pred. No. 69; Length 411 7; Indels Indels NON_TER 1 1 1 1 1 NON_TER 411 411 SEQUENCE 411 AA: 44302 MW; 043EBA65BF8984C1 CRC64; Pfam: PF02386; TrkH: 1. SEQUENCE 550 AA: 61950 MW: 4BADFCAE2BC85441 CRC64; 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) Last sequence update)
Last annotation update) Score 41; DB 8; Pred. No. 50; 8; Mismatches 550 AA Mismatches Interpro: IPR000194; ATPase alpha_beta. Interpro: IPR000790; ATPase_A_C. 01-oCT-2000 (TrEMBLrel. 15, Created) Created) PRT; 389 RGARLTEVPKQQQYEPLPIEK 409 1 RAARISLGPRXYSFKPMPLXR 21 41.0%; 28.6%; Ouery Match
Best Local Similarity 57.18;
Matches 8; Conservative AAF17042.1; 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17, Best Local Similarity 28.6 Matches 6; Conservative PRELIMINARY; PRELIMINARY; M162.7. Caenorhabditis elegans 6 SLGPRXYSFKPMPL 19 81 K+-NA+ SYMPORTER HKT1. SEQUENCE FROM N.A. TISSUE-YOUNG STEM; EMBL; AF197710; M162.7 PROTEIN. Mitochondrion. 01-OCT-2000 Query Match O9XUC6; **09LLM4 09LLM4** 93nx60

RESULT
100 09 100
AC 09 100
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. COLUMBIA; TISSUE-WHOLE SEEDLINGS AT LEAF STAGE 2;
Davenport R.J., Kiegle E.A., Tester M.;
"GLRS, an ionotropic glutamate receptor ortholog from Arabidopsis.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF210701; AAF21042.1;
InterPro; IPR0011311; SBP_glut_receptor.
InterPro; IPR001132; Ion_glut_receptor.
InterPro; IPR001828; ANF_receptor.
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41.0%; Score 41; DB 5; Length 690; 47.4%; Pred. No. 88;
                                                          Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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55.6%; Pred. No. 1.2e+02;
tive . 1; Mismatches 5
                                                                                                                                                                                                                                                                                                          921 AA.
                                                    2; Mismatches
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Job time: 985 sec

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(without alignments)
3.575 Million cell updates/sec
                                                                                                                            February 27, 2002, 11:36:02; Search time 132.19 Seconds
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                               212252 seqs, 22503292 residues
                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                       1 RAARISLGPRXYSFKPMPLXR 21
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                   ~100
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length: 0 length: 2000000000 Post-processing: Minimum Match 0% Minimum DB seq Maximum DB seq

Total number of hits satisfying chosen parameters:

/cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* Maximum Match 100% Listing first 45 summaries Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Sequence 3, Appli Sequence 3, Appli Sequence 10, Appli Sequence 7, Appli Appl Appli Appl Appli Appl Sequence 10, Sequence 2 Description Sequence 7 Sequence 1 Sequence 2 Sequence 7 Sequence 1 Sequence Sequence Sequence Sequence Sequence Sequence Seguence Sequence Sequence US-09-246-5008-10 US-08-299-285-10 US-08-299-285-10 US-08-296-126-7 US-08-965-126-7 US-08-965-126-7 PCT-US95-11126-7 PCT-US95-11126-7 US-08-985-126-5 US-08-985-126-13 PCT-US95-11126-5 PCT-US95-11126-13 PCT-US95-11126-14 US-09-246-500B-14 US-08-781-562-6 US-08-299-285-5 US-08-299-285-13 US-08-299-285-14 US-08-299-285-23 US-08-985-126-14 US-08-985-126-23 SUMMARIES Match Length Score Result

Seque.	Sequence	Sequence 10,	Sequence 8, App.	8,	Sequence 3, Appli	6	12,	6	4, 1	Sequence 7, Appli	7, 1	7,	Sequence 11, Appl	12,	Sequence 12, Appl	Sequence 12, Appl	Sequence 1, Appli
US-09-246-500B-12	US-07-637-870-5	US-07-640-476-10	US-07-637-399-8	US-08-112-703-8	US-07-637-870-3	US-07-637-399-9	US-07-640-476-12	US-08-112-703-9	US-07-637-870-4	US-07-637-399-7	US-07-640-476-7	US-08-112-703-7	US-07-640-476-11	US-08-299-285-12	US-08-985-126-12	PCT-US95-11126-12	US-07-641-346B-1
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74	347	347	348	348	387	387	387	387	388	388	388	388	389	10	10	10	154
38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	37.0	37.0	37.0	37.0
38	38	38	38	38	38	38	38	38	38	38	38	38	38	37	37	37	37
28	29	30	31	32	33	. 34	35	36	37	38	39	40	41	4.2	43	44	4.5

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: van Oostrum, Jan
APPLICANT: Boyar, william C,
APPLICANT: Boyar, william C,
APPLICANT: Galakatos, Nicholas G,
APPLICANT: Schmitz, Albert
APPLICANT: Schmitz, Albert
TITLE OF INVENTION: C5a Receptor Antagonists Having
TITLE OF INVENTION: C5a Spaceptor Antagonists Having
TITLE OF INVENTION: C5a Spaceptor Antagonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STRRET: 600 South Avenue West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Kelease #1.0, Version #1.25
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/08/A63,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASS FICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FOLEY, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
TELEX: 139-125
                         Sequence 3, Application US/08463224
Patent No. 5807824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-224-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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US-08-463-224-3
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                      CITY: 1
STATE:
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DB 1; Length 74; 0.19; Indels Query Match

48.0%; Score 48; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 10; Conservative 0; Mismatches

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Gaps

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1 RAARISLGPR 10 ò

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GENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: CTerminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 1; Length 10;
Pred. No. 0.22;
0; Mismatches 2; Indels
                                                                                                                                  Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FURW:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPOTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/U8/29,285
FILING DATE: 31-AUG(-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Red 1/2 AUG(-1994
TELEPHONE/COCKET NUMBER: 36,252
REFERENCE/COCKET NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEPAX: (215) 563-404
INFORMATION EN GID: SEQUENCE CHRARCTERISTICS:
FENETH: UN AMINO ACIDS
FENETH: UN AMINO ACIDS
FENETH: UN AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
STATE: PA
                                                                                                                                    ore 48; DB 4;
red. No. 0.19;
Mismatches C
                                                                                                                                48.0%; Score 48;
100.0%; Pred. No.
:ive 0; Mismatcl
GRGANISM: Human C5a Anaphylatoxin
FEATURE:
NAME/KEY: CARBOHYD
LOCATION: (64)...(66)
US-09-246-500B-10
                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08299285 Patent No. 5696230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: not relevant
not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 42.0
Best Local Similarity 80.0
Matches 8; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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37 RAARISLGPR 46
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                                                                                      Sequence 3, Application US/08463377
Patent No. 5837499
GENERAL INFORMATION:
APPLICANT: Wan Oostrum, Jan
APPLICANT: Boyar, William C.
APPLICANT: Schultz, Albert
APPLICANT: Schultz, Albert
APPLICANT: Schultz, Albert
TITLE OF INVENTION: C5a Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5837499Agonist Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
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STREET: 600 South Avenue West
CITY: Westfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
0.19;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
8.09-246-500B-10
5.Sequence 10, Application US/09246500B
7.Patent No. 6235494
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100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: FOLEY, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 139-125
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 48.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-463-377-3
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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37 RAARISLGPR 46
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  37 RAARISLGPR 46
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                                                                                                                                                                                                                                                                                                                                                                                                                              21P: 07090
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                                                        RESULT 2
US-08-463-377-3
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Gaps

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CORRESPONDENCE ADDRESS:
                                                                                                        COUNTRY: US
ZIP: 19103-2307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-985-126-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY:
                              Sequence 10, Application US/08299285
Patent No. 5696230
GENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: T-EPHEN High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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APPLICANT: Sherman, Simon A.
APPLICANT: Rirnarsky, Leonid
APPLICANT: Taylor: Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 1; Length 10; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER REALBABLE FURNER:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Jatentin Release #1.0, Version #1.30
SOFTWARE: Jatentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/29,285
FELECATION: S30
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 63075
FELECOMMUNICATION NUMBER: 63075
FELECOMMUNICATION INFORMATION:
TELEPAN: (215) 563-404
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: "D-Alanine at position 9" US-08-299-285-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
امت 8: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                     CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YSFKDMPLAR 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-08-299-285-24
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
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Gaps
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APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPPRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: "D-Alanine at position 9" US-08-299-285-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                        FILING DATE: 31-AUG-1994
CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: RECALL JANGER: 36,252
RECISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
COUNTRY: US
Z1P: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC:COOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/08985126 Patent No. 5942599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.08;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 42.0
Best Local Similarity 80.0
Matches 8; Conservative
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Sequence 24, Application US/08985126
Parent No. 5942599
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.0%; Score 42; DB 2; Length 10; 80.0%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 9 OTHER INFORMATION: "D-Alanine at position 9" US-08-985-126-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
ATTONEY/AGENT INFORMATION:
RACHISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                  SS: single
No. 5942599 Relevant
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TELECOMMUNICATION INFORMATION:
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TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Modified-site
                                                                                                                                                                                                                              MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: C-terminal
                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 80.0
Matches 8; Conservative
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                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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ZIP: 19103-2307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sanderson, Sam D.
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Dann, Dorfman, Herrell and Skillman: 1601 Market Street Suite 720
Philadelphia
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Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUBER:
FLING DATE: 31-40G-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERRECPOCKET NUMBER: 63075
TELEPROME (215) 563-4100
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
FILING DATE:
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APPLICATION NUMBER: US/08/299,285
FILING DATE: 31.AUG-1994
ATTORNEY/AGENT INFORMATION:
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2.IP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08985126 Patent No. 5942599
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TELEPHONE: (215) 563-4100
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 80.v
B: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YSFKDMPLAR 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FRAGMENT TYPE:
US-08-985-126-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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US-08-985-126-10
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ANTI-SENSE: NO FRAGMENT TYPE: C-terminal

us-09-446-109a-5.rai

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: Treminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADORESS:
ADDRESSEE: Dann, Dociman, Herrell and Skillman, P.C.
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
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.; OTHER INFORMATION: /product= "D-Alanine at position 9"
PCT-US95-11126-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 5;
Pred. No. 0.22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US95-11126-24
Sequence 24, Application PC/TUS9511126
Sequence 12, Application PC/TUS9511126
POPLICANT: Sanderson, Sam D.
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 63075 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sanderson, Sam D. Sherman, Simon A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (215) 563-4100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.00,
"whas 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (215) 563-4044 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SS: single
not relevant
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LENGTH: 10 amino acids
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12 YSFKPMPLXR 21

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Gaps
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APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 1; Length 10; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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APPLICATION NUMBER: US/08/299,285 FILING DATE: 31-AUG-1994
CLASSIFICATION: 530
                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285 FILING DATE: 31-AUG-1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEE: Dann, Dorfman, Herrell and Skillman F: 1601 Market Street Sulte 720 Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               CLASSIFICATION: JOHN ATTORNEY/ACENT INFORMATION:
NAME: Reed, Janet E.
REGIESTRATION NUMBER: 36, 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/08299285 Patent No. 5696230 GENERAL INFORMATION:
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NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 6307
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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O
                                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SS: not relevant
not relevant
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80.0%;
                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C-terminal
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ZIP: 19103-2307
COMPUTER READABLE FORM:
                                                                              ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
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APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
WIMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
TITLE OF INVENTION: High Affinity Response-Selective TITLE OF INVENTION: High Affinity Response-Selective TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann. Dealer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . LOCATION: 9
. OTHER INFORMATION: /product= "D-Alanine at position 9"
PCT-US95-11126-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 5; Length 10; Pred. No. 0.22;
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                                                                                                                                                             3: Dann, Dorfman, Herrell and Skillman, P.C.
1601 Market Street Suite 720
                                                                                                                                                                                                                                                                    ZIP: 19103-2307
COMPUTER-RENDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (215) 563-410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 5, Application US/08299285
; Patent No. 5696230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SS: not relevant not relevant
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80.0%;
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Philadelphia
                                                                                                                                                                                                            Philadelphia
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STRANDEDNESS: not
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US-08-299-285-5
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APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
WUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.0%; Score 41; DB 1; Length 10; 80.0%; Pred. No. 0.33; 2; Indels live 0; Mismatches 2; Indels
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COUNTRY: US
2 IP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: "D-Phenylalanine at OTHER INFORMATION: position 9" US-08-299-285-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 5942599 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/08985126
Patent No. 5942599
GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4044
INPORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLEGULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: NO: 5942599 Re
                                                                                                                                                                                                                                        ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                       NAME/KEY: Modified-site LOCATION: 9
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Best Local Similarity 80.0
Matches 8; Conservative
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US-08-985-126-5
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TOPOLOGY: No. 5942599 Relevant

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

MANTI-SENSE: NO

JERAGMENT TYPE: C-terminal

US-08-985-126-5

Ouery Match

Best Local Similarity 80.0%; Pred. No. 0.33;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 YSFKPMPLXR 21

III | | | | | | | | |

Db 1 YSFKDMPLGR 10

Search Completed: February 27, 2002, 11:36:03

Job time: 142 sec
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C-terminal truncat C-terminal truncat C-terminal truncat C-terminal truncat C-terminal truncat C-terminal truncat Human complement C Human complement C

Human anaphylatoxi Human C5a protein. Human C5a anaphyla Human C5a. Homo s

complement c Human complement C

Human Human Human

AAB74095 AAB74096 AAW07785 AAW07786 AAW07789 AAW07789 AAW07789 AAW07789 AAW07789 AAW07789 AAW07789 AAW07789 AAW07789 AAW07790 AAW07791 AAW07791 AAW07791 AAW07791 AAW07791 AAW07791 AAW07791 AAW07791

Variant human CSa. Mouse CSa anaphyla Pro-CS polypeptide H. pylori GHPO 109

AAB74119 AAE05458 AAR77604 AAW98761 AAB74063 AAB74090

AAB74066 AAB74093 AAB74095 AAR94487 AAR94470

C-terminal truncat C-terminal truncat C-terminal truncat C-terminal truncat C-terminal truncat C-terminal truncat C5a anaphylatoxin

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/note- "Serum amyloid A is attached to the N-terminal"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Aminohexanoic acid which is a linear aliphatic spacer moiety"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 11 /note= "D-form residue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW27254 standard; peptide; 12 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US16825
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                                                                                                                                                                                                                                                                           1676
Modified-site
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AAW27254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AAW27254
Molecular adjuvant
Molecular adjuvant
Molecular adjuvant
Molecular adjuvant
Human C5a peptide
C-terminal truncat
Human C5a peptide
                                                                                        (without alignments)
4.881 Million cell updates/sec
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                                                                            February 27, 2002, 11:41:14 ; Search time 303.5 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                  / SIDS8/gcgdata/geneseq/Aa1980.DAT: *
/ SIDS8/gcgdata/geneseq/geneseqp/Aa1980.DAT: *
/ SIDS8/gcgdata/geneseqg/geneseqp/Aa1990.DAT: *
/ SIDS8/gcgdata/geneseqg/geneseqp/Aa1991.DAT: *
/ SIDS8/gcgdata/geneseqg/geneseqp/Aa1992.DAT: *
/ SIDS8/gcgdata/geneseq/geneseqp/Aa1992.DAT: *
/ SIDS8/gcgdata/geneseqg/geneseqp/Aa1995.DAT: *
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/SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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          4.5
Compugen Ltd
                                                                                                                                                                                                                               Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                         522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
         GenCore version Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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AAW27251
AAW27250
AAW27256
AAB74086
AAB74086
AAB74084
AAB74084
AAB74083
AAB74083
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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WPI; 1997-244854/22
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                                                                                                                                                  A novel molecular adjuvant has been developed for enhancing an immune response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ligand being functionally linked to the immunogen, and so binding of the molecular adjuvant to the APC determinant activates the APC, effecting delivery of the sequence ropresents a specifically claimed formula for a molecular adjuvant, where the immunogen is serum amyloid A. The molecular adjuvant can be used to produce an immune response for protecting against viral and other pathogens or to produce anti-tumour responses. It can also be
                                                                                                                                                                                                                                                                                                    used for the production of antibodies for use as immunodiagnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and processed by APCs to provide APC-mediated immune responses. It can provide for the production of antibodies against a weakly antigenic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular adjuvant; immune response; immunogen; binding affinity; antigen presenting cell; APC; viral pathogen; anti tumour response; antibody; immunodiagnostic; immunotherapeutic; agonist.
                                                                         Molecular adjuvants for enhancing immune responses - comprise an immunogen linked to a ligand having binding affinity for a determinant of an antigen presenting cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
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                        Tempero RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW27251 standard; peptide; 19 AA
                          Sanderson SD,
                                                                                                                             Claim 15; Page 53; 61pp; English
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                                                                                                                                                                                                                                                                                                                                                         non-antigenic substances
(UYNE-) UNIV NEBRASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNE-) UNIV NEBRASKA.
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Best Local Similarity
Matches 11; Conserv
                      Hollingsworth MA,
                                                                                                                                                                                                                                                                                                                                                                                 12 AA;
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response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ligand being functionally linked to the immunogen, and so binding of the molecular adjuvant to the APC determinant activates the APC, effecting delivery of the immunogen to an antigen presenting pathway of the APC. The present immunogen to an antigen presenting pathway of the APC. The present sequence represents a specifically claimed targeting ligand and immunogen. The molecular adjuvant can be used to produce an immune produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodaingnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and processed agents. The molecular adjuvant is readily taken up and processed control of antibodies dgainst a weakly-antigenic or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular adjuvant; immune response; immunogen; binding affinity; antigen presenting cell; APC; viral pathogen; anti tumour response; antibody; immunodiagnostic; immunotherapeutic; agonist.
Molecular adjuvants for enhancing immune responses - comprise an immunogen linked to a ligand having binding affinity for a determinant of an antigen presenting cell
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                                                                                         Claim 6; Page 52; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.5%;
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Best Local Similarity 57.9
Matches 11; Conservative
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ò \$; response to an immunogen. The molecular adjuvant comprises a targeting aligand, having binding affinity for a characteristic determinant of an antigan presenting cell (APC), the targeting ligand being functionally linked to the immunogen, and so binding of the molecular adjuvant to maning a ctivates the APC, effecting delivery of the timmunogen to an antigen presenting pathway of the APC. The present sequence represents a specifically claimed targeting ligand, which is a CSa C-terminal decapeptide agonist. The molecular adjuvant can be used to produce an immune response for protecting against viral and other pathogens or to produce antitumour responses. It can also be used for immunotherapeutic agents. The molecular adjuvant taken up and processed by APCs to provide APC-mediated immune responses. It can approvide for the production of antibodies against a weakly-antigenic or A novel molecular adjuvant has been developed for enhancing an immune Gaps Molecular adjuvant; immune response; immunogen; binding affinity; antigen presenting cell; APC; viral pathogen; anti tumour response; antibody; immunodiagnostic; immunotherapeutic; agonist. Molecular adjuvants for enhancing immune responses - comprise an immunogen linked to a ligand having binding affinity for a .; 0 Score 50; DB 18; Length 10; 1; Indels Molecular adjuvant targeting ligand and immunogen. Pred. No. 0.026; Tempero RA; 0; Mismatches determinant of an antigen presenting cell determinant of an antigen presenting cell /note- "D-form residue" Location/Qualifiers Example 1; Page 31; 61pp; English. AAW27256 standard; peptide; 18 AA Sanderson SD, Claim 5; Page 51; 61pp; English. 50.5%; 96WO-US16825 95US-0005727 23-DEC-1997 (first entry) Best Local Similarity 90.0 Matches 9; Conservative (UYNE-) UNIV NEBRASKA. WPI; 1997-244854/22. 11 YSFKPMPLXR 20 Hollingsworth MA, Misc-difference WO9714426-A1 18-OCT-1996; 20-OCT-1995; 24-APR-1997 Synthetic Sequence AAW27256: Query Match RESULT AAW27256 ò

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response to an immunogen. The molecular adjuvant comprises a targeting ligand, having binding affinity for a characteristic determinant of an antigen presenting cell (APC), the targeting ligand being functionally inked to the immunogen, and so binding of the molecular adjuvant to the APC determinant activates the APC, effecting delivery of the immunogen to an antigen presenting pathway of the APC. The present sequence represents a targeting ligand and immunogen, in which the juxta-membrane epitope of human mucin-1 is positioned toward the carboxyl terminus and the C5a analogue is positioned toward the amino terminus. The molecular adjuvant can be used to produce an immune produce anti-tumour responses. It can also be used for the production of antibodies for use as immunodiagnostic and immunotherapeutic agents. The molecular adjuvant is readily taken up and processed by APCs to provide APC-mediated immune responses. It can provide contribution of antibodies against a weakly-antigenic or
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novel molecular adjuvant has been developed for enhancing an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; C5a; complement; antibody; bacterial infection; sinusitis; meningitis; respiratory; gastrointestinal; urinary tract infection;
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Pred. No. 0.05;
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Best Local Similarity 90.vv
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The present sequence is a C-terminal truncated C5a peptide fragment. The present invention relates to an antibody specific for the present sequence. The C5a-antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or urinary tract infections or infections in wounds. In addition, the C5a antibody can be used for treating sepsis. C5a is also known as
                                                                                                                                                                                                                                                                                                                                      meningitis; respiratory; gastrointestinal; urinary tract infection; wound; anaphylatoxin; sepsis.
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                                                                                                                                                                                                                                                                                                        C5a; complement; antibody; bacterial infection; sinusitis;
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                                                                                                                                                                                                                                              C-terminal truncated C5a peptide #23
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                                                                   AAB74085 standard; Peptide; 16 AA.
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Best Local Similarity
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sinusitis, meningitis, respiratory, gastrointestinal or urinary tract
infections or infections in wounds. In addition, the C5a antibody can
be used for treating sepsis. C5a is also known as anaphylatoxin.
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                                                                                                                                                                                                   Score 47; DB 22; Length 9;
Pred. No. 4.3e+05;
0; Mismatches 0; Indels
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Matches 9; Conservative
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antibodies generated against C-terminal truncated C5a peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compositions for treating blood-borne and toxin mediated diseases and treatment of sepsis in humans and other animals comprises anti-C5a
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                                                                                                                                  Compositions for treating blood-borne and toxin mediated diseases etreatment of sepsis in humans and other animals comprises anti-C5a antibodies generated against C-terminal truncated C5a peptides
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                                                                                                                                                                        Disclosure; Page 29; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                   AAB74083 standard; Peptide; 18 AA
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                                                         99US-0387671
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Best Local Similarity 100.
Matches 9; Conservative
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                                                                                               Huber-Lang M,
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                                                                            (UNMI ) UNIV MICHIGAN
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                                                                                                                WPI; 2001-226665/23
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WO200115731-A1.
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                                                                                                                                                                                                                                                             anaphylatoxin.
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                                      31-AUG-2000;
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                    08-MAR-2001
                                                                                              Ward PA,
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                                      The present sequence is a C-terminal truncated C5a peptide fragment. The present invention relates to an antibody specific for the present sequence. The C5a antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or uninary tract infections or infections: in wounds. In addition, the C5a antibody can be used for treating sepsis. C5a is also known as
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0.16;
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Disclosure; Page 29; 84pp; English.
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100.0%;
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                                                                                                                                                                                                                                                                                                             18 AA;
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AAB74054

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The present sequence is a C-terminal truncated C5a peptide fragment. The present invention relates to an antibody specific for the present sequence. The C5a-antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or urinary tract infections or infections in wounds. In addition, the C5a antibody can be used for treating sepsis. C5a is also known as
                                                                        C5a; complement; antibody; bacterial infection; sinusitis; meningitis; respiratory; gastrointestinal; urinary tract infection; wound; anaphylatoxin; sepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitis; respiratory; gastrointestinal; urinary tract infection; wound; anaphylatoxin; sepsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibodies generated against C-terminal truncated C5a peptides
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0.18;
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0; Mismatches
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Pred. No.
                                        C-terminal truncated C5a peptide #25
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     16-MAY-2001 (first entry)
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Best Local Similarity
"Thes 9; Conserv?
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                                        Gaps
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meningitis; respiratory; gastrointestinal; urinary tract infection;
wound; anaphylatoxin; sepsis.
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47.5%; Score 47; DB 22; Length 19; 100.0%; Pred. No. 0.17; 1.ive 0; Mismatches 0; Indels
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Best Local Similarity 100.08; Pr
Harrhes 9; Conservative 0;
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                                                                                                                                                                                                                                                                                                         Human C5a peptide fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-AUG-2000; 2000WO-US24219.
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 Query Match 47.5
Best Local Similarity 100.
Matches 9; Conservative
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N-PSDB; AAF75792.
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The present sequence is a C-terminal truncated C5a peptide fragment. The present invention relates to an antibody specific for the present sequence. The C5a-antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial
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urinary tract infections or infections in wounds. In addition, the C5a
antibody can be used for treating sepsis. C5a is also known as
sequence. The C5a-antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial infection, e.g. sinusitis, meningitis, respiratory, gastrointestinal or urinary tract infections or infections in wounds. In addition, the C5a antibody can be used for treating sepsis. C5a is also known as
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meningitis; respiratory; gastrointestinal; urinary tract infection;
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0; Mismatches 0
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0.18;
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0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                             The present sequence is a C-terminal truncated C5a peptide fragment. The present invention relates to an antibody specific for the present sequence. The C5a-antibody can be used in a therapeutic composition, which is useful for treating a subject suffering from bacterial
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urinary tract infections or infections in wounds. In addition, the CSa
antibody can be used for treating sepsis. CSa is also known as
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0.18;
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                                                                                                                                                                                                                                      Disclosure; Page 29; 84pp; English
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les 9; Conservative
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A; Introns: 139/3; 246/3; 487/3; 784/1; 960/2; 1067/3; 1113/3; 1171/3; 1321/2; 1383/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein A360R - Chlorella virus PBCV-1
C.Species: T12860
C.Species: T17860
R.Species: T17860
A.Steference number: Z18806
A.Steferences: EMBL:U42580; NID:g4028896; PIDN:AAC96728.1
A.Steferences: EMBL:U42580; NID:g4028896; PIDN:AAC96728.1
A.Steferences: EMBL:U42580; NID:g4028896; PIDN:AAC96728.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ### Species Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: To-oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27684
A:Thomas, K.
Submitted to the EMBL Data Library, March 1996
A:Reference number: 220404
A:Reference number: 220404
A:Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 8.9;
4; Mismatches
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T23097
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A; Residues: 1-2219 <WIL.>
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A; Map position:
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                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                    Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                             219241 seqs, 76174552 residues
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                                                                                                                                          February 27, 2002, 11:45:16
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Maximum Match 100%
Listing first 45 summaries
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R.Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKe son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997
A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A.Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A.Reference number: A64520; MUID:97394467
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A:Residues: 1-1279 <TOM>
A:Cross-references: GB:AE000649; CB:AE000511; NID:g2314687; PIDN:AAD08556.1; PID:g231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type IIS restriction enzyme R and M protein - Helicobacter pylori (strain 26695)
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C:Species: Caenorhabditis elegans
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C:Species: Caenorhabditis elegans
C:Accession: T25043
R:Baynes. C.
R:Baynes. C.
A:Reference number: 219973
A:Reference number: 219973
A:Reference number: 219973
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Rolecule type: DNA
A:Residues: 1-1170 cMLL>
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C:Genetics: C.
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45.5%; Pred. No. 9;
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C: Superfamily: alpha-2-macroglobulin
C: Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; if
C: Superfamily: alpha-2-macroglobulin
C: Keywords: complement alternate pathway; complement pathway; cytolysis; glycoprotein; if
F: 1-18/Domain: signal sequence *status predicted <S1G>
F: 19-673,678-1676/Product: complement C5 *status predicted <C5B>
F: 19-673,752-1676/Product: complement C5 alpha chain *status predicted <C5B>
F: 678-1676/Product: complement C5 alpha chain *status predicted <C5A>
F: 752-1676/Product: complement C5 alpha chain *status predicted <C5A>
F: 752-1676/Product: c5a anaphylatoxin *status experimental <C5T>
F: 752-1676/Product: c5a anaphylatoxin *status predicted <C5B>
F: 752-1676/Product: c5a anaphylatoxin *status predicted <C5B>
F: 751-752-1676/Product: c5a anaphylatoxin *status predicted <C5B>
F: 751-752-1676/Product: c5a anaphylatoxin *status experimental *status experimental *status predicted <S11,1115,1630/Binding site: carbohydrate (Asn) (covalent) *status experimental *status predicted <S11,1115,1630/Binding site: carbohydrate (Asn) (covalent) *status experimental *status predicted <S11,1115,1630/Binding site: carbohydrate (Asn) (covalent) *status experimental *status predicted <S11,1115,1630/Binding site: carbohydrate (Asn) (covalent) *status experimental *status *status
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A:Residues: 1-1676 <HAV>
A:Residues: 1-1676 <HAV>
A:Cross-references: GB-M57729; NID:g179982; PIDN:AAA51925.1; PID:g179983
A:Note: 518-Ser was also found
A:Note: 518-Ser was also found
B:Wetsel, R.A.; Lemons, R.S.; Le Beau, M.M.; Barnum, S.R.; Noack, D.; Tack, B.F.
Biochemistry 27, 1474-1482, 1988
A:Title: Molecular analysis of human complement component C5: localization of the struct
A:Reference number: A27689; MUID:88209511
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A: Residues: 412-1676 <WET>
A: Residues: 412-1676 <WET>
A: Residues: 412-1676 <WET>
A: Cross-references: GB: M65134; GB: M18879; NID: 9179691; PIDN: AAA51856.1; PID: 9179692
A: Cross-references: GB: M65134; GB: M18879; NID: 9179691; PIDN: AAA51856.1; PID: 9179692
A: Title: Primary structural analysis of the polypeptide portion of human C5a anaphylatox
A: Reference number: A01267
A: Molecule type: protein
A: Residues: 678-751 
A: 
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C:Comment: Activation of C5 initiates the spontaneous assembly of the late complement of C:Comment: Activation of C5 initiates the spontaneous assembly of the late complement of C:Comment: C5a has potent spasmogenic and chemotactic activity.
C:Cenetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Title: Complete cDNA sequence of human complement pro-C5. Evidence of truncated transca A:Reference number: A40075; MUID:91079575
A:Accession: A40075
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A: Residues: 412-854, SLALSPRLECNGKISGHCKLRLPGSSDSPASASOVAGITGTHHHAQPT' <LUN>
A: Residues: 412-854, SLALSPRLECNGKISGHCKLRLPGSSDSPASASOVAGITGTHHHAQPT' <LUN>
A: Cross-references: GB:K02874
A: Note: the carboxyl-terminal part of the sequence in this report appears to be derived R: Bohnsack, J.F.; Mollison, K.W.; Buko, A.M.; Ashworth, J.C.; Hill, H.R.
Biochem, J. 273, 635-640, 1991
A: Title: Group B streptococci inactivate complement component C5a by enzymic cleavage at A: Contents: annotation
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                                                                                                                                                                                                                                                                                                                                                                                                    complement C5 precursor (validated) · human
N:Contains: C5a anaphylatoxin; C5b
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 08-Dec-2000
C;Accession::A40075; A27689; A01267; A01266; S15121
R:Haviland, D.L.; Haviland, J.C.; Fleischer, D.T.; Hunt, A.; Wetsel, R.A.
J. Immunol. 146, 362-368, 1991
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                                                                                            666 YKHVLENLKRISSFKPLPFER 686
2 YKHSV--VKKXYSFKPMPLXR 20
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probable iron-sulfur protein Cj0074c [imported] • Campylobacter jejuni (strain NCTC l C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000 C;Accession: D81423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ryparkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A; Reference number: A81250; MUID:20150912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AL139074; GB:AL111168; NID:96967505; PIDN:CAB72560.1; PID:9696
A;Experimental source: serotype O2, strain NCTC 11168
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     C:Comment: This inhibitor is involved in protection against exogenous enzymes resembl C;Superfamily: cystatin; cystatin homology C;Keywords: cysteine proteinase inhibitor; seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Helianthus annuus (common sunflower)
C.Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: JE0308
R;Doi-Kawano, K; Kouzuma, Y.; Yamasaki, N.; Kimura, M.
J; Biochem. 124, 911-916, 1998
A;Title: Molecular cloning, functional expression, and mutagenesis of A;Reference number: JE0308; MUID:99011314
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                                                                                                                                           Length 101;
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Pred. No. 19;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 cysteine proteinase inhibitor · common sunflower
                                                                                                                                             Score 42; DB
Pred. No. 3.6;
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                                                                                                                                                                                               3; Mismatches
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47.4%; Pred. No.
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A; Residues: 1-123 <DOI>
C; Superfamily: cystatin; cystatin homology
                                                                                                                                             42.48;
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ilarity 58.3%;
Conservative
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Best Local Similarity 47.4%
Matches 9; Conservative
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449 VIKKWYAFKELP 460
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Best Local Similarity
These 7; Conserve
                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
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J. Blochem. 119, 1106-1113, 1996
A; Title: Purification, characterization, and sequencing of two cysteine proteinase inhit A; Reference number: JC4791; MUD:96424994
A; Accession: JC4792
A; Molecule type: protein
A; Residues: 1-101 < KQU>
A; Experimental source: seed
hypothetical protein UU474 [imported] - Ureaplasma urealyticum C:Species: Ureaplasma urealyticum C:Species: Ureaplasma urealyticum C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 %Accession: 68280.

R:Glass, J.L.; Lefkowitz, E.J.; Glass, J.S.; Helner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000 A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir A:Accession: 682887 A:Status: preliminary A:Accession: 682887 A:Status: DNA A:Molecule type: DNA A:Residues: jr:313 GLA> A:Coss references: GB-AE002143; GB:AF222894; NID:g6899457; PIDN:AAF30886.1; GSPDB:GN001 A:Experimental source: serovar 3; blovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
E72672
E72672
E72672
C;Potetical protein APE0803 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 08-Sep-2000
C;Accession: E72672
E;Kawarabayasi, Y.: Hino, Y.: Horikawa, H.: Yamazaki, S.: Haikawa, Y.: Jin-no, K.: Takat awa, H.: Takamiya, M.: Masuda, S.: Funahashi, T.: Tanaka, T.: Kudoh, Y.: Yamazaki, J.: K DN Res 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A:Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79781.1; PID:d1043567; PID:9510
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C;Species: Hellanthus annuus (common sunflower)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 07-May-1999
C;Accession: JC4792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: APE0803
C;Superfamily: Aeropyrum pernix hypothetical protein APE0803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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Pred. No.
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Matches 8; Conservative
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Best Local Similarity 63.6
Matches 7; Conservative
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49 KHTILKKYYSF 59
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A; Molecule type: DNA
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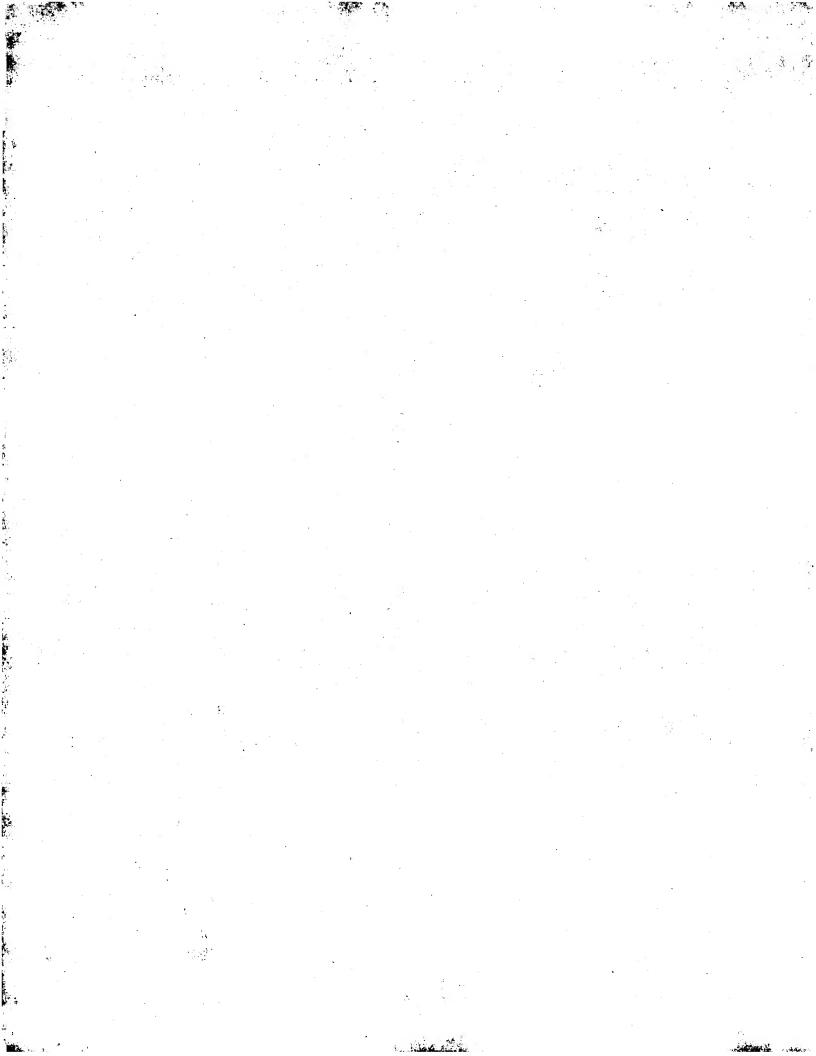
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C;Accession: T05038
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Sch submitted to the Protein Sequence Database, February 1998
A;Reference number: 215395
A;Reference number: 215395
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                          C;Accession: F8214
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488
A;Accession: F85214
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A;Molecule type: DNA
A;Residues: 1-566 CSTO>
A;Cross-references: GB:NC_001268; NID:97268695; PIDN:CAB78903.1; GSPDB;GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4-commarate--CoA ligase homolog F13C5.180 - Arabidopsis thaliana (fragment) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                              4-coumarate-CoA ligase-like [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb_2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
                                                                 Gaps
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C;Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
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                 Length 370;
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A;Cross-references: EMBL:AL021711
A;Experimental source: cultivar Columbia; BAC clone F13C5
               Score 41; DB 2;
Pred. No. 22;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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Pred. No. 34;
6; Mismatches
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A;Introns: 356/3; 420/1; 468/3; 491/2; 525/3
A;Note: F13C5.180
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Pred. No.
               Ouery Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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Best Local Similarity 35.3%;
Matches 6; Conservative
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186 YSIMKESFGFVPKPLIK 202
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186 YSIMKESFGFVPKPLIK 202
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Best Local Similarity 35.3.
6. Conservative
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20 SVVQKSHGFVPSPL 33
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JED291
FB19 protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: JED291
C;Accession: JED291
R;Totaro. A.; Grifa, A.; Carella, M.; Rommens, J.M.; Valentino, M.A.; Roetto, A.; Zelant Biochem. Blophys. Res. Commun. 250, 555-557, 1998
A;Title: Cloning of a new gene (FB19) within HLA class I region.
A;Reference number: JED291; MUID:99003493
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C:Kcywords: chloroplast
F:1-57/Domain: transit peptide (chloroplast) #status predicted <TNP>
F:58-370/Product: peridinin-chlorophyll a-binding protein #status predicted <MAT>
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El protein - cottontail rabbit papillomavirus
C:Species: cottontail rabbit papillomavirus
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 24-Feb-1994
C:Accession: A0357
R:Giri, I: Danos, O.; Yaniv, M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985
A;Title: Genomic structure of the cottontail rabbit (Shope) papillomavirus.
A:Reference number: A94027; MUID:85166175
A;Holccule type: DNA
A;Holccule type: DNA
A;Holccule type: CIR>
C;Superfamily: papillomavirus El protein
C;Keywords: early:protein
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A:Residues: 1-940 <TOT>
A:Cross-references: GB:Y13247; NID:92117158; PIDN:CAA73697.1; PID:92117159
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24;
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39;
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Pred. No.
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53.38;
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Matches 7; Conservative
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Matches 8; Conservative
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A; Residues: 1-370 <SHA>
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A;Gene: FB19
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us-09-446-109a-6.rsp

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Compugen Ltd.
 GenCore version Copyright (c) 1993 - 2000
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 protein search, using sw model OM protein

February 27, 2002, 11:42:43; Search time 78.39 Seconds Run on:

(without alignments) 9.354 Million cell updates/sec

US-09-446-109A-6

1 KYKHSVVKKXYSFKPMPLXR 20 Title: Perfect score Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

144 homo sapien	60 rattus norv	14 mus musculu	191 homo sapien	130 equine herp	550 rattus norv	668 aquifex aeo	q8 cyanidium c	23 odontogloss	90 odontogloss	35 odontogloss	129 aquifex aeo
P291	064560	0645	0141	. P244	980d .	2190	. 09tl	0841	P225	0841	6.490
TPP2_HUMAN	TPP2_RAT	TPP2_MOUSE	WRN_HUMAN	VGLH_HSVE4	CO5A_RAT	RL5_AQUAE	HIS5_CYACA	MOVP_ORSVC	MOVP_ORSVJ	MOVP_ORSVS	MOAA_AQUAE
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1249	1249	1262	1432	852	16	188	214	303	303	303	320
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=79005687; PubMed=690134; Fernandez H.N., Hugli T.E.; Pernandez H.N., Hugli T.E.; Pernandez H.N., Hugli T.E.; Pernany structural analysis of the polypeptide portion of human C5a anaphylatoxin. Polypeptide sequence determination and assignment of the oligosaccharide attendment site in C5a."; Biol. Chem. 253:6955-6964(1978).
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Lundwall A.B., Wetsel R.A., Kristensen T., Whitehead A.S.,
Woods D.E., Ogden R.C., Colten H.R., Tack B.F.;
"Isolation and sequence analysis of a cDNA clone encoding the fifth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haviland D.L., Haviland J.C., Fleischer D.T., Hunt A., Wetsel R.A., "Complete coDNs sequence of human complement pro-C5. Evidence of truncated transcripts derived from a single copy gene.", J. Immunol. 146:362-368(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular analysis of human complement component C5: Localization the structural gene to chromosome 9.\text{\ensuremath{\text{n}}};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-88309754; PubMed-3408713;
Zuiderweg E.R.P., Mollison K.W., Henkin J., Carter G.W.;
"Sequence-specific assignments in the 1H NMR spectrum of the human
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 412-1676 FROM N.A.
MEDLINE-88209511; Pubmed-3365401;
Wetsel R.A., Lemons R.S., Lebeau M.M., Barnum S.R., Noack D.,
                                                                                                          21-JUL-1986 (Rel. 01, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2011 (Rel. 40, Last annotation update)
COMPLEMENT C5 PRECURSOR [CONTAINS: C5A ANAPHYLATOXIN].
                                       1676 AA
                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement component.";
J. Biol. Chem. 260:2108-2112(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91079575; PubMed=1984448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 27:1474-1482(1988)
                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF C5A.
                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 678-751.
                               CO5_HUMAN
P01031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tack B.F
CO5_HUMAN
                                           HAN KERTAN KERTA
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MEDLINE-96424994; PubMed-8827445;
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"Purification, characterization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1676 AA; 188331 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00287; CYSTATIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00031; cystatiń; l.
ProDom; PD001231; Cystatin.
SMART; SM00043; CY; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 9; Conservative
 Pfam; PF01835; A2M_N; 1.
Pfam; PF01821; ANATO; 1.
Pfam; PF01759; NTR; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heliantheae; Helianthus.
NCBI_TaxID=4232;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTB_HELAN
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                              PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               010993;
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CHAIN
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                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONVERTANCE OF TOWN PROTEOLYTIC DECRADATION OF COMPLEMENT CS, CS ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDUCES THE CONTRACTION OF SMOOTH WUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND BASOPHILIC LEUKOCYTES. GSA ALSO STIMULATES THE LOCOMOTION OF POLYMORPHONUCLEAR LEUKOCYTES (CHEMOKINESIS) AND DIRECT THEIR MIGRATION TOWARD SITES OF INFLAMMATION (CHEMOTAXIS).
SUBUNIT: C5 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 BASIC RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE BOND. C5 CONVERTASE ACTIVATES C5 BY CLEAVING THE ALPHA CHAIN, ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SIMILARITY: TO C3, C4 AND ALPHA-2-MACROGLOBULIN.
-:- SIMILARITY: CONTAINS 1 ANAPHYLATOXIN-LIKE DOMAIN.
-:- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 855
                                                                                                                                                                                                                                    "Heteronuclear three-dimensional NMR spectroscopy of the inflammatory
                                                   STRUCTURE BY NMR OF C5A.
MEDLINE-89207527; PubMed-2784981;
Sulderweg E.R.P., Nettesheim D.G., Mollison K.W., Carter G.W.;
"Tertiary structure of human complement component C5a in solution from nuclear magnetic resonance data.";
Biochemistry 28:172-185(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang X., Boyar W., Toth M.J., Wennogle L., Gonnella N.C., *Structural definition of the C5a C terminus by two-dimensional
                                                                                                                                                                                                                                                                                                                                              Zhang X., Boyar W., Galakatos N., Gonnella N.C.;
"Solution structure of a unique C5a semi-synthetic antagonist:
Implications in receptor binding.";
Protein Sci. 6:65-72(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ONWARD DUE TO THE PRESENCE OF AN ALU REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001599; Alpha_2_macroglobln.
InterPro; IPR000020; Anaphylatoxin.
InterPro; IPR001840; Anaphylatoxn.
                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF C5A.
MEDLINE-97160477; Pubmed-9007977;
                                                                                                                                                                              STRUCTURE BY NMR OF C5A.
MEDLINE=89274164; PubMed=2730871;
Zuiderweg, E.R.P., Fesik S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF C5A.
MEDLINE-97332508; PubMed-9188742;
protein C5a.";
27:3568-3580(1988).
                                                                                                                                                                                                                                                                          Blochemistry 28:2387-2391(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M57729; AAA51925.1; -.
EMBL; M65134; AAA51856.1; -.
PIR; A40075; C5HU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002890; A2M_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00207; A2M; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1KJS; 15-MAY-97
1CFA; 17-SEP-97
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                                                                                                                                                                                                                                                         protein C5a.";
inflammatory
Biochemistry
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J. Biochem. 119:1106-1113(1996).
-!- FUNCTION: STRONG INHIBITOR OF PAPAIN, FICIN AND CATHEPSIN H, B AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
                                                                                                                          Complement pathway; Complement alternate pathway; Glycoprotein; Plasma; Membrane attack complex; Cytolysis; Inflammatory response; Signal; Polymorphism; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.5%; Score 47; DB 1; Length 1676; 100.0%; Pred. No. 4.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_001996.
w; 87DCAA65FF977D19 CRC64;
                                                                                                                                                                                                                                                                                                                                                             COMPLEMENT C5 ALPHA CHAIN
                                                                                                                                                                                                                                                                                        COMPLEMENT C5 BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE TYPE 1 CYSTATIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB).
PRINTS; PRO0004; ANAPHYLATOXN.
SMART; SMO0104; ANATO; 1.
PROSITE; PSO0477; ALPHA_2_MACROGLOBULIN; FALSE_NEG.
PROSITE; PSO1177; ANAPHYLATOXIN_1; 1.
PROSITE; PSO1178; ANAPHYLATOXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANAPHYLATOXIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                        C5A ANAPHYLATOXIN.
C5B (ALPHA').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helianthus annuus (Common sunflower).
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InterPro; IPR000010; Cystatin.
InterPro; IPR003243; Cystatin_C_M.
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VASOACTIVE INTESTINAL PEPTIDE PRECURSOR (VIP)
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Best Local Similarity 35.0
Matches 7; Conservative
                       Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 1
85 1
200 AA;
                                                                                                                                                                                                                  SEQUENCE OF 129-156
                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A01551; VRCH
                                                                   NCBI_TaxID=9031;
                                                                                                          TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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                                                                                                                                                                                                                                                                                                                         MEDLINE-85166175; Pubmed-2984661;
MEDLINE-85166175; Pubmed-2984661;
Giri I., Danos O., Yaniv M.;
"Genomic Structure of the cottontail rabbit (Shope) papillomavirus.";
Proc. Natl. Acad. Sci. U.S.A. 82:1580-1584(1985).
- I FUNTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF VIRAL DNA REPLICATION IT FORMS A COMPLEX WITH THE VIRAL E2 PROTEIN. THE BLE COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH CONTAINS BINDING SITES FOR BOTH PROTEINS.
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00524; E1_N: 1. Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
                                                                                                                                                                                                                                                               Cottontail rabbit (shope) papillomavirus (strain Kansas) (CRPV).
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                      5
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0
                                             Score 42; DB 1; Length 101; Pred. No. 1.7; 5; Indels 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 1; Length 602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 438 ATP (POTENTIAL).
602 AA; 67943 MW; 239EF0F3F627D6A5 CRC64;
          101 AA; 11186 MW; 789CD3E9611CBFD1 CRC64;
                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1998 (Rel. 36, Last annotation update)
REPLICATION PROTEIN El.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIP_CHICK STANDARD; PRT; 200 AA. P4814; P01285; 21-JU-1986 (Rel. 01, Created) PFB-1996 (Rel. 33, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                               602 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 11;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; K02708; -; NOT_ANNOTATED_CDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A03657; WIWLRB.
InterPro; IPR001177; Papillom_E1.
                                             42.4%;
ilarity 47.4%;
Conservative
                                                                                                          85 WKHS--KKLLGFKPAPVDK 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.48;
                                                                                            2 YKHSVVKKXYSFKPMPLXR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.88;
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Thiol protease inhibitor. SEQUENCE 101 AA; 11186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 YKHSVVKKXYSFKPMP 17
                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00519; E1; 1.
                                                        Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein.
NP_BIND 431
SEQUENCE 602 AA;
                                                                                                                                                                                                                                                                                         Papillomavirus.
NCBI_TaxID-31553;
                                                                                                                                                                              VE1_CRPVK
P03112;
                                               Query Match
                                                          Best Loca
Matches
                                                                                                                                                      RESULT 4
VIP_CHICK
ID VIP_C
AC P4814
DT 21-JU
DT 01-FE
DT 15-DE
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Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure of the vasoactive intestinal octacosapeptide from chicken intestine. The amino acid sequence."; FEBS Lett. 60:322-326(1975).
                                                                                                                                                                                                               McFarlin D.R., Lehn D.A., Moran S.M., Macdonald M.J., Epstein M.L.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VASOACTIVE INTESTINAL PEPTIDE.
AMIDATION (G-157 PROVIDE AMIDE GROUP).
MISSING (IN SHORT ISOFORM).
902A88F998CAB402 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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PRINTS; PR00275; GLUCAGON.

SMART: SM00070; GLUCA; 2.

PROSITE; PS002060; GLUCAGON; 1.

Glucagon family; Cleavage on pair of basic residues; Signal;

Amidation; Hormone; Alternative splicing.

POTEWTIAL.

POTEWTIAL.
                                                                                                                                                                                                                                                                                                                                         TISSUE-Hypothalamus;
Talbot R.T., Dunn I.C., Wilson P.W., Sang H.M., Sharp P.J.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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-!- FUNCTION: PHI ALSO CAUSES VASODILATION.
-!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.4%; Score 41; DB 1;
35.0%; Pred. No. 5.2;
iive 6; Mismatches 7
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                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-84 AND 120-200 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-76210823; PubMed-1227973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000532; Glucagon.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
MM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.48;
57.18;
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286
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370 AA;
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family;
TRANSIT
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ID COS_MOUSE
AC P06684;
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REPEAT
REPEAT
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                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria: Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTESTINAL PEPTIDE PHI-27.
VASOACTIVE INTESTINAL PEPTIDE.
AMIDATION (G-157 PROVIDE AMIDE GROUP).
B159313495273F06D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCP1_AMPCA STANDARD; PRT; 370 AA.
904048; PS1872;
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PERIDININ-CHILOROPHYLL A PROTEIN I PRECURSOR (PCP).
Amphidinium carterae (Dinoflagellate).
Eukaryota: Alveolata: Dinophyceae; Gymnodiniales; Gymnodiniaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00260; GLUCAGON; 1.
Glucagon family; Cleavage on pair of basic residues; Signal;
Amidation; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.4%; Score 41; DB 1; Length 200 35.0%; Pred. No. 5.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                         FUNCTION: PHI ALSO CAUSES VASODILATION.
SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
                                            01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VASOACTIVE INTESTINAL PEPTIDE PRECURSOR (VIP)
        200 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                  Meleagris gallopavo (Common turkey)
        PRT;
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9
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InterPro; IPR000532; Glucagon.
Pfam; PF00123; hormone2; 2.
PRINTS; PR00275; GLUCAGON.
SMART; SM00070; GLUCAG. 2.
                                  Created)
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        STANDARD;
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1115
156
156
                              01-NOV-1995 (Rel. 32, 01-NOV-1995 (Rel. 32, 15-DEC-1998 (Rel. 37,
                                                                                                                                                                                                                                                                                                                 AND GALL BLADDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
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                                                                                                                                      NCBI_TaxID=9103;
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        VIP_MELGA
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SEQUENCE
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SIGNAL

1_AMPCA

RESULT
PCP1_AM
FOR 1 DP
FOR 1 DP
FOR 1 DP
FOR 1 DP
FOR 2 DP
FOR 3 DP
FOR 3

Matches

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VIP_MELGA
DT VIP_MELGA
DT O1-NO
DT 15-DE
DE VASOA
GN NELDA
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                                                                                                                                                                                                                                                                                                                                                                                  "Structural basis of light harvesting by carotenoids: peridinin-
chlorophyll-protein from Amphidinium carterae.";
Science 272:1788-1791(1996).
-!- FUNCTION: WATER-SOLUBLE ANTENNA FOR CAPTURE OF SOLAR ENERGY IN THE
BLUE-GREEN RANGE. PERIDININ IS AN ASYMMETRIC CAROTENOID HAVING A
MAXIMUM ABSORPTION AT APPROXIMATELY 480 NM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBUNIT: HOMOTRIMER.
-!- DOMAIN: THE MATURE PROTEIN IS COMPOSED OF 2 ALMOST IDENTICAL
MEDILINE-96413810; PubMed-8816945;
Sharples F.P., Wrench P.M., Ou K., Hiller R.G.;
"Two distinct forms of the peridinin-chlorophyll a-protein from
Amphidinium carterae.";
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-> T (IN REF. 1; CAA64242).

-> I (IN REF. 1; AA SEQUENCE).

-> E (IN REF. 1; AA SEQUENCE).

7F113EB0DD8F372E CRC64;
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20-AUG-2001 (Rel. 40, Last annotation update)
COMPLEMENT C5 PRECURSOR (HEMOLYTIC COMPLEMENT) [CONTAINS: C5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERIDININ-CHLOROPHYLL A PROTEIN CHLOROPHYLL A-BINDING. CHLOROPHYLL A-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light-harvesting polypeptide; Transit peptide; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41; DB 1; Length 370;
Pred. No. 9.7;
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                                                                                                                                                                   Biochim. Biophys. Acta 1276:117-123(1996).
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                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE-96256477; Pubmed-8650577;
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MOVP_PMMVJ
P89658;
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                                                                         CARBOHYD
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MOVP_PMMVJ
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Wetsel R.A., Ogeta R.T., Teck B.E.;

Brochemistry 26:137-43(1987).

Brochemistry 26:137-43(1987).

C.!-FUNCTION: ACTIVATION OF C5 BY A C5 CONVERTASE INITIATES THE SPONTANEOUS ASSEMBLY OF THE LATE COMPLEMENT COMPONENTS, C5-C9, INTO THE MEMBRANE ATTACK COMPLEX. C5B HAS A TRANSIENT BINDING SITE FOR C6. THE C5B-C6 COMPLEX IS THE FOUNDATION UPON WHICH THE LYTIC COMPLEX IS ASSEMBLED.

COMPLEX INTERPRETED.

COMPLEX IS ASSEMBLED.

COMPLEX IS ASSEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute of Decinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                  SEQUENCE FROM N.A.
MEDLINE-90153853; PubMed-2303408;
Wetsel R.A., Fleischer D.T., Haviland D.L.;
"Deficiency of the murine flucoplement component (C5). A 2-base pair gene deletion in a 5'-exon.";
J. Biol. Chem. 265:2435-2440(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PSOU477; ALPHA_1, MACROCLOBULIN; FALSE_NEG.
PROSITE; PSO1177; ANAPHYLATOXIN_1; 1.
PROSITE; PSO1177; ANAPHYLATOXIN_2; 1.
Complement pathway; Complement alternate pathway; Glycoprotein;
Plasma; Membrane attack complex; Cytolysis; Inflammatory response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENT CS ALPHA CHAIN.
CSA ANAPHYLATOXIN.
CSB (ALPHA').
ANAPHYLATOXIN-LIKE.
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InterPro; IPR002890; A2M_N.
InterPro; IPR001599; Alpha_2_macroglobin.
InterPro; IPR000020; Anaphylatoxin.
InterPro; IPR001840; Anaphylatoxin.
InterPro; IPR001134; Netrin_C.
InterPro; IPR001134; Netrin_C.
InterPro; IPR001134; Netrin_C.
IPRam: PF01835; A2M_N: 1.
IPRam: PF01835; A2M_N: 1.
IPRam: PF01835; A7M_N: 1.
IPRam: PF01859; NTR: 1.
                                                                                                                                                             SEQUENCE OF 41-1680 FROM N.A.
MEDLINE-87185363; PubMed-2436653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0004; ANAPHYLATOXN.
SMART; SM00104; ANATO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M3525; AAA37349.1; -. EMBL; M35226; AAA37348.1; -. PIR; A27538; A27538. HSPIR; A35530. HSSP; P01031; IKJS.
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NCBI_TaxID=10090;
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PEPTIDE
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SIGNAL
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"Nucleotide sequence of the Japanese isolate of pepper [Capsicum annuul mild mottle tobamovirus ("WV-P) RNA.";
Ann. Phytopathol. Soc. Jpn. 63:373-376(1997).
-!- FUNCTION: INVOLVED IN TRANSPORT OF THE VIRUS FROM THE INITIALLY INFECTED CELLS TO ADJACENT CELLS, POSSIBLY BY MODIFYING THE FUNCTION OF THE PLASMODESMATA. ALSO INFLUENCES LOCAL LESION.
DEVELOPMENT. BINDS TO SINGLE-STRANDED NUCLEIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MOVEMENT PROTEIN (CELL-TO-CELL TRANSPORT PROTEIN) (30 KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pepper mild mottle virus (strain Japan) (PMMV-J).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
NCBI_TaxID=138663;
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
Y -> L (IN DEFECTIVE VARIANT CSD).
MISSING (IN DEFECTIVE VARIANT CSD).
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                                                                                                                                                                                                                                                                           Score 41; DB 1; Length 1680;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40; DB 1; Length 257; Pred. No. 10; 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                        81EBSA16FAC7D95C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28345 MW; 9F375F2E691FB0A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ā
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Pfam; PF01107; Tobamo_MP; 1.
PRINTS; PR00964; MOVEMENT.
                                                                                                                                                                                                        AA; 188877 MW;
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                                                                                                                                                                                                                                                                             41.4%;
88.9%;
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Best Local Similarity 88.9،
نہم 8; Conservative
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108 YRTSAAKKRFAFKLIP 123
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735
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915
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216
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SEQUENCE 257 AA; 28
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693 KYKHSVPKK 701
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    702
703
715
427
915
11119
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DPOA_RAT
089042;
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                                                                                                                                                                                           Gaps
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"Molecular cloning and nucleotide sequence of deer papillomavirus.";
J. Virol. 56:85-91(1985).
J. Virol. 56:87-91(1985).
VIRAL DIA REPLICATION IT FORMS A COMPLEX WITH THE VIRAL E2
PROTEIN THE BILE COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
CONTAINS BINDING SITES FOR BOTH PROTEINS.
                01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MOVEMENT PROTEIN (CELL-TO-CELL TRANSPORT PROTEIN) (30 KDA PROTEIN).
                                                                                                                   Pepper mild mottle virus (strain Spain) (PWMV-S).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
NCBL_TaxID=31745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28345 MW; 75903246CED872AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986 (Rel. 01, Created)
01-FBE-1996 (Rel. 33, Last sequence update)
12-JUL-1998 (Rel. 36, Last annotation update)
REPLICATION PROTEIN E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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MEDLINE-85293253; Pubmed-2993669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J01314; WMTMP3.
rPro; IPR001022; Tobamo_MP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M81413; AAB02336.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01107; Tobamo_MP; 1. PRINTS; PR00964; MOVEMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |: | || ::|| :|
108 YRTSAAKKRFAFKLIP 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding; Transport
SEQUENCE 257 AA; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10564;
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PO3117;
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DPT DPT B DP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                       InterPro: IPR001177; Papillom_E1.
Pfam; PF00519; E1: 1.
Pfam; PF00524; E1.N: 1.
Early protein; DNA replication; Helicase; ATP-binding; DNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Popanda O., Flohr C., Thielmann H.W.; A mutation in the gene of subunit II of DNA polymerase alpha from Novikoff cells is conconitant with altered physico-chemical properties of the enzyme."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: POLYMERASE ALPHA IN A COMPLEX WITH DNA PRIMASE IS A REPLICATIVE POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA POLYMERASE ALPHA CATALYTIC SUBUNIT (EC 2.7.7.7) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.4%; Score 39; DB 1; Length 613; 50.0%; Pred. No. 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          440 447 ATP (POTENTIAL).
613 AA; 68076 MW; E177124381837BCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1451 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ011605; CAA09720.1; -. InterPro; IPR002064; DNA_pol_B. Pfam; PF00136; DNA_pol_B; 1.
                                                                                                                                                                                                                                                                          EMBL; M11910; AAA66843.1; -.
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Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 YKHSVVKKXYSFKPMP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                            PIR; A03664; W1WLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116;
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MormPep; C06E1.7; CE00062
                                                                                                                                                                                  DNA-binding;
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P34302:
                                                                                                                                                                                                             DNA_BIND
VARIANT
                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: NUCLEAR.

MISCELLAMEDUS: IN EURARYOTES THERE ARE FIVE DNA POLYMERASES:
ALPHA, BETA, CAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR
DIFFERENT REACTIONS OF DNA SYNTHESIS.
MISCELLAMEDUS: CONSERVED REGIONS II, IV, III AND I ARE THOUGHT TO
BE INVOLVED IN SUBSTRATE RECOGNITION, BINDING OR PP(I) HYDROLYSIS:
SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ween the Swiss institute of Bioinformatics and the EMBL outstati
European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT PHE-1180.
WEDLINE-94171797; PubMed-8125989;
MEDLINE-94171797; PubMed-8125989;
Izumi M., Miyazawa H., Harakawa S., Yatagai F., Hanaoka F.;
Izumi M., Miyazawa H., Harakawa S., Yatagai F., Hanaoka F.;
Identification of a point mutation in the cDNA of the catalytic subunit of DNA polymerase alpha from a temperature-sensitive mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning of the cDNAs for the four subunits of mouse DNA bolymerase alpha-primase complex and their gene expression during cell proliferation and the cell cycle.";
J. Biol. Chem. 268:8111-8122(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FM3A Cell line.";
J. Biol. Chem. 269:7639-7644(1994).
-i- FUNCTION: POLYMERASE ALPHA IN A COMPLEX WITH DNA PRIMASE IS A
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyazawa H., Izumi M., Tada S., Takada R., Masutani M., Ui M.,
                                                                                                                               Score 39; DB 1; Length 1451;
Pred. No. 89;
        PROSITE: PS00116; DNA_POLYMERASE_B; 1.
Transferase: DNA-directed DNA polymerase; DNA replication;
DNA-binding; Nuclear protein POTENTIAL.
DNA_BIND 657 722
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 454-472 AND 1438-1455 MEDLINE-93216788; Pubmed-8463324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stadibauer F., Brueckner A., Rehfuess C., Eckerskorn C., Lottspeich F., Foerster V., Tsang B.Y., Nasheuer H.P.; "DNA replication in vitro by recombinant DNA-polymerase-alpha-primase-"."

Eur. J. Blochem. 222:781-793(1994).
                                                                                                                                                          3; Indels
                                                                                        1451 AA; 165305 MW; FOEIB16F8B8D5CD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE N PYROPHOSPHATE + DNA(N).
                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DNA POLYMERASE ALPHA CATALYTIC SUBUNIT (EC 2.7.7.7).
                                                                                                                                                                                                                                                                             PRT; 1465 AA.
                                                                                                                                                         5; Mismatches
                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-94298818; Pubmed-8026492;
                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-JUN-1994 (Rel. 29, Last seq
                                                                                                                               39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPLICATIVE POLYMERASE.
                                                                                                                 Ouery Match.
Best Local Similarity 42.5.
Best Local Similarity 42.5.
SM00486; POLBC; 1
                                                                                                                                                                                                                                                                             STANDARD;
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436 KFKSKIVEKNYAFE 449
                                                                           1451
                                                                                                                                                                                   1 KYKHSVVKKXYSFK 14
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                              1252
1451
                                                                                                                                                                                                                                                                                                                                                         POLA OR POLA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hanaoka F.;
                                                                                                                                                                                                                                                                             DPOA_MOUSE
P33609;
                                                 DNA_BIND
DNA_BIND
NON_TER
SEQUENCE
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Evilon L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Materson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                          SMARY; SM0486; POLBC; 1.
PROSITE; PS00116; DNA_POLYMERASE_B; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
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29, Last annotation update)
KDA PROTEIN C06E1.7 IN CHROMOSOME III.
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5; Mismatches
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Rhabditidae; Peloderinae; Caenorhabditis
                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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MEDLINE=94150718; Pubmed=7906398;
                                                                                                                       EMBL, D13543; BAA40003.1; -. BMBL, D17364; BAA04202.1; -. PIR: S45628; S45628. MGD; MGI:99660; Polal. InterPro; IPR002064; DNA_POL_B. Pfam: PF00136; DNA_POL_B: 1. PRINTS; PR00106; DNAPOLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1465 AA; 167339 MW;
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Best Local Similarity 42.9%;
Matches 6; Conservative
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01-FEB-1994 (Rel. 2)
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HYPOTHETICAL 41.7 KI
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P18569;
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                                                                                                                                                                                  MTR_NEUCR STANDARD; PRT; 470 AA.
1918680;
10.1FGB-1995 (Rel. 31, Created)
10.1NOV-1997 (Rel. 35, Last sequence update)
10.1NOV-1997 (Rel. 35, Last annotation update)
10.1NOV-1997 (Rel. 35, Last annotation update)
10.1NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurospora crassa.";
Genome 34:644-651(1991).
-!- FUNCTION: REQUIRED FOR THE TRANSPORT OF NEUTRAL ALIPHATIC AND
AROMATIC AMINO ACIDS VIA THE N SYSTEM.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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                                                                                        <u>ب</u>
                                                                                                                                                                                                                                                                                    Eukaryota: Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   'Sequence and structure of mtr, an amino acid transport gene
                                                                  Length 363;
                                                                                        Indels
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                        11 protein.
363 AA; 41747 MW; 824336C2101EED3C CRC64;
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                                                                 38.9%; Score 38.5; DB 1; 45.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport; Amino-acid transport; Transmembrane.
DOMAIN 1 56 EXTRACELLULAR (POT
                                                                                       1; Mismatches
InterPro; IPR002516; Glycosyl_transf_ll.
Pypam; PF01511; Glyco_transf_ll; l.
Hypothetical protein.
SEQUENCE 363 AA: 41747 MW; 824336721
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Pfam; PF01490; Aa_trans: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                          | 121 | SECULENCE OF 210-470 FROM N.A. | MEDLINE-92146948; PubMed-1838345; | NOO K., Stuart W.D.
                                                                                                                                                                                                                                                                                                                                         STRAIN-OAK RIDGE;
MEDLINE-95095055; PubMed-8001794;
                                                                                                                        174 KYKEKVQSFVKPAIDFSPLP 193
                                                                                                           1 KYKHSV---VKKXYSFKPMP 17
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                                                                           Best Local Similarity 45.0
Matches 9; Conservative
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MTR_NEUCR
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"Identification and characterization of lef-1, a baculovirus gene involved in late and very late gene expression.";
J. Virol. 67:3481-3488(1993).
-!- FUNCTION: CATALYZES THE TRANSFER OF GLUCOSE FROM UDP-GLUCOSE TO ECTYSTEROIDS WHICH ARE INSECT MOUTING HORMONES. EXPRESSION OF EGT INTERFERES WITH NORMAL INSECT DEVELOPMENT AND BLOCK MOLTING.
-!- SIMILARITY: BELONGS TO THE UDP-GLYCOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Reilly D.R., Miller L.K.;
"A baculovirus blocks insect molting by producing ecdysteroid UDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D., "The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                   ö
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01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ECDYSTEROID UDP-GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Autographa californica nuclear polyhedrosis virus (ACMNPV).
Viruses: dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                   Score 38; DB 1; Length 470;
Pred. No. 41;
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                     CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
E8132D1A62373300 CRC64;
                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Μ
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43.8%;
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Virology 202:586-605(1994).
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454 RYDHGKVSKPYSCAPL 469
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296
316
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Best Local Similarity
7; Conserva
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470 AA;
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                                                                                                                         C EMBL; M22619; AAA69845.1; ...

R EMBL; M96361: AAA66785.1; ...

R EMBL; L09723; AAA66785.1; ...

R EMBL; L22888; AAA66645.1; ...

DR INCEPPCO: IL2888; AAA66645.1; ...

DR PIR; A34314; XUNVAC.

DR PROSTTE; PS003213; UDPGT.

DR PROSTTE; PS00375; UDPGT: 1.

DR PROSTTE; PS00375; UDPGT: 1.

FT Transferase; Glycosyltransferase; Signal.

FT SIGNAL

FT CHAIN 19 506 ECDYSTEROID UDP-GLUCOSYLTRANSFERASE.
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Gaps

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Score 38; DB 1; Length 506; Pred. No. 45; 5; Mismatches 4; Indels

Query Match
Best Local Similarity 35.7%;
Matches 5; Conservative

1 KYKHSVVKKXYSFK 14 :|:| ::|| | 465 RYRHDISRQLYSLK 478

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Search completed: February 27, 2002, 11:42:44 Job time: 543 sec

049414 arabidopsis 019149 ceenorhabdi 09179 drosophila 021997 streptococc 067015 aquifex aeo 09416 letsimania 094h18 yaba-11ke d 094h1 pseudomonas 09471 drandida alb 07471 candida alb 09471 candida alb 09470 candida alb 09170 caenorhabdi 099725 bacceriopha 099725 bacceriopha

09hw87 pseudomonas 087138 vibric chol P7448 vibric chol 046216 drosophila 062618 drosophila 022311 caenorhabdi 09x1k1 thermotoga

Q99h23 heliocoverp Q9ska6 arabidopsis **09ssw4 oryza sativ**

OM protein

Run on:

Sequence:

Searched:

Database

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Paramecium bursaria chlorella virus 1 (PBCV-1).
Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
NCBI_TaxID=10506;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-95133167; Pubmed-7831789;

Lu Z., Li Y., Zhang Y., Kutish G.F., Rock D.L., Van Etten J.L.;

Lu Z., Li Y., Zhang Y., Kutish G.F., Rock D.L., Van Etten J.L.;

"Analysis of 45 kb of DNA located at the left end of the chlorella virus PBCV-1 genome.";

virology 206:339-332(1995).

EMBL; U4280; AAC967281; --.

SEQUENCE 241 AA; 26311 MW; A47481C943BE5015 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 12; Length 241; Pred. No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Indels
                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last Sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
GENOME, PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                            241 AA
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                                                                                 074714
Q9UW20
001470
Q99MWB
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Q9AYZ5
Q9S3X0
Q99HZ3
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Q9SSW4
Q9HW87
049414
Q19149
Q9VL79
021997
067015
Q9U1F3
Q9DHI8
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P74948
046216
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21 FKRSVVKKPLGIKPLPARR 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 51.5
Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                           PRELIMINARY;
566
498
498
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084674;
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084674
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                                                                                                                                                                                                                                                                                                              084674 paramecium O9n505 caenorhabdi 021388 caenorhabdi 026046 helicobacte 022624 caenorhabdi 09pqi ureaplasma 09yqu aeropyun p 09grt7 leishmania 09yf54 aleutian mi 09yj2 drosophila 09ick9 cottontail 09ick9 cottontail 09ick9 cottontail 055000 rattus norv
                                                                         (without alignments)
10.383 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                 February 27, 2002, 11:50:06; Search time 281.76 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                    473505 seqs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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09N505
02N388
0256046
022624
09PC016
09YR57
09FR77
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
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sp_organelle:*
sp_phage:*
                                                                                                US-09-446-109A-6
                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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42.5
42
42
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Gaps

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01-0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2000 (TrEMBLrel. 15, Last annotation update) HYPOTHETICAL PROTEIN Y40C7B.5.

AC DT DT DT DT COS OS

000405 homo sapien Q9vw47 drosophila Q9gph4 drosophila Q9fpw2 amphidInium

Q9GPH4 Q9FPW2

09VW47

Result ş Caenorhabditis elegans

610 AA

PRELIMINARY;

Q9N505 Q9N505;

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PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 388:539-547(1997)
                                                                                                                   Ouery Match
Best Local Similarity
Matches 10; Conserva
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Matches 10; Conserv
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MEDLINE-94150718; PubMed-7906398;

MEDLINE-94150718; PubMed-7906398;

MEDLINE-94150718; PubMed-7906398;

MA Mison R., Ainscough R., Anderson K., Baynes C., Berks M.,

MA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,

MA Grafner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

MA Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Sanders D., Shownkeen R.,

RA Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Materston R.,

RA Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,

RA Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.;

RY 12.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Indels
                                                                                                                                                                                                                                                                                                                   Jones K., Tin-Wollam A., Yoakum M.;
"The sequence of C. elegans cosmid Y40C7B.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AC006757; AAF60545.1; -
SEQUENCE 610 AA; 70271 MW; D7C2063F77457816 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB
Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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InterPro: IPRO00169; Thiolprot_act_site.
InterPro: IPR00957; ZnF_NFX1.
InterPro: IPR003015; HbLMyc.
                                                                                         SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.5%;
50.0%;
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Best Local Similarity
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J. Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                 Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the gastric pathogen Helicobacter
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                                                                                                          Length 2219;
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SMART; SM00438; ZNE_NFX; 4.
SEQUENCE 2219 AA; 253649 MW; F0F5A0F37D04EDOC CRC64;
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PROSTIE; PS00092; N6_MTASE; UKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 1279 AA: 149714 MW; 5838BF4E242A7A31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TYPE IIS RESTRICTION ENZYME R AND M PROTEIN (ECO57IR).
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
T21B10.3
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23;
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Pred. No.
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01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-JUN-2001 (TrEMBLrel. 17, Last anno
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MEDLINE-99310339; PubMed-10382966; Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Junno K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Juno K., Takahai M., Sekine M., Baba S.-I., Ankai A., Kosugi H., Takamiya M., Makuda S., Ruahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix KI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leishmania mexicana.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiese M., Wany Q., Goercke I.;
"Identification of mitogen-activated protein (MAP) kinases from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1579;
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ293286; CAC07962.1;
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR001245; Tyr_kin.
InterPro; IPR001245; Tyr_kin.
SMART; SM00220; S-TKc; 1.
SMART; SM00219; TyrKc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
ULMAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE MITGGEN-ACTIVATED PROTEIN KINASE 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 5; Pred. No. 1.1e+02; 3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1579 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165702 MW;
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Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 SVVKKXYSFKPMPLXR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=MNYC/BZ/62/M379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 VVKKXYSFKPMP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1579 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 VVKGTYSLKPLP
                                                                                SEQUENCE FROM N.A
                        NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
   Aeropyrum
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09YR54
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Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceac; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.4%; Score 44; DB 2; Length 1313; 63.6%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1170;
                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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EMBL: AE002143; AAF30886.1; -.
Hypothetical protein; Complete protecme.
SEQUENCE 1313 AA: 150068 WW: B3625ABAA5997F91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     93.2; -.
135532 MW; 461F6BA1A2B6BF04 CRC64;
                                                                                                                                             Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL PROTEIN UU474.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 36.8 KDA PROTEIN APE0803.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.5%; Score 45; DB 44.4%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SEROVAR 3;
MEDLINE-20500219; Pubmed-11048724;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                          investigating biology.";
Science'282;2012-2018(1998).
EMBL; 268318; CAA92693.2; --
SEQUENCE 1170 AA: 135532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 KYSYSLCKDYYRWKELPL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KYKHSVVKKXYSFKPMPL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 63.6
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                      SEQUENCE FROM N.A.
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Archaea; Crenarch
                                 NCBI_TaxID=6239
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O9YDW6
ID Q9
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DT 01
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CM APP
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Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Holf W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Beson K.Y., Benos P.V., Berman B.P., Brandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Bullke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Durbin K.J., Evangelista C.C., Ferriacr S., Pleischmann W.,
R. Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li H., Post A.F., "The nitrate assimilation genes of the diazotrophic, bloom-forming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNAY-2000 (TrEMBLrel. 17, Last annotation update)
BG: DSO4929.3 PROTEIN.
BG: DSO4929.3 ROGISZ89.
BC: DSO4929.3 AROGISZ89.
BC: DSO4929.3 AROGISZ89.
Eukaryota melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.4%; Score 42; DB 2; Length 510; 36.8%; Pred. No. 53; tive 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cyanobacterium Trichodesmium strain WH9601.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF178846; AAF00916.1;
InterPro; IPR000660; Nir Sir.
Pfam; PF01077; NIR_SIR; I.
PRINTS; PR00397; SIROHARM.
PROSTITE; PR00365; NIR_SIR; I.
SEQUENCE 510 AA; 57584 MW; F3ED188E0BC8619F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Cyanobacteria; Oscillatoriales; Trichodesmium
                                                                                                                                                                                                                             01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
FERREDOXIN NITRITE REDUCTASE.
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                                                                                                                                                510 AA.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        Trichodesmium sp. WH9601.
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Matches 7; Conservative
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449 VIKKWYAFKELP 460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WH9601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                            09RA39;
                                                                                                                                             Q9RA39
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                                                                                   RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
                                                                                                                                                                                                                                                                                                                                                                        Mejerland T., Belak S.;
"Unusual high genetic diversity of Aleutian mink disease virus.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFIO7634; AAD04600.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NCTC 11168.

BEDLINE-20150912: PubMed-10688204;

Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,

Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,

Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,

Ouail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                                                                                   Aleutian mink disease virus.
Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
NCBI_TaxID=28314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                  Olofsson: A.: Mittelholzer C., Treiberg Berndtsson L., Lind L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112 AA; 13052 MW; ODFBAC185243FF6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54220 MW; 3BB1885D5CFD9BF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0cT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE IRON-SULFUR PROTEIN.
                                                 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-WAR-2001 (TrEMBLrel. 16, Last annotation update) NONSTRUCTURAL PROTEIN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42.5; DB 12;
Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
2
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50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00037; fer4; 2.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
PROSITE; PS00018; EF_HAND; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL139074; CAB72560.1; -.
InterPro; IPR001450; 4FE4S_ferrdxin.
InterPro; IPR002048; EF-hand.
                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reveals hypervariable sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.48;
58.38;
                  01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KYKHSVVKKXYSFKPMPL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 58.37
F. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 403:665-668(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nonstructural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVKKXYSFKPMP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
SEQUENCE 479 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                   STRAIN-El;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
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09PJ47

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Mismatches
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"CRPVa4 complete nucleotide sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.4%; Score 42;
53.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Allen P.B., Ouimet C.C., Greengard P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 papillomavirus
           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92828 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 0:0-0(1998).
EMBL, AF040954, AAB96775.1; -
InterPro; IPR000571; Zf-CCCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TFS2_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00509; TFS2N; 1.
SMART; SM00356; ZnF_C3H1; 1.
                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 YKRAMVSGVFSYGPMP 290
                                                                                                                       275 YKRAMVSGVFSYGPMP 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 YKHSVVKKXYSFKPMP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
                                                                              2 YKHSVVKKXYSFKPMP 17
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 872 AA; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
'... 7; Couserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A4 COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E1.
Cottontail rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                                                                                                                                                                                                                                                          Q91CK9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
                                                                                                                                                                                                                                                          RESULT · 14
           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            055000
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                                                                                                                                                                                                                                                                                 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Ra Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert Ki., Remington K., Sanders R.D.C., Scheeler F., Shen H., Shue B.C.; Sfden Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Smith T., A. Spier E., Yacton R., Strong R., Sun E., Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Nang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., A. Weinstock G.M., Weissenbach J., A. Weinstock G.M., Weissenbach J., A. Weinstong K.C., Wul D., Yang S., Yao Q.A., A. Weinstong R., Zhon M., Zhong K., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;;
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Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McCleod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .:
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63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
COTTONTAIL RABBIT PAPILLOMAVIRUS SUBTYPE B COMPLETE GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 5; Length 593;
Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Metal-binding; Nuclear protein; Zinc-finger.
593 AA; 64409 MW; 347CE5F8138B2EE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SUBTYPE B;
Salmon J., Orth G., Breitburd F.;
"Complete nucleotide sequences of the CRPVb strain.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ242187; CAB96116.1;
InterPro: IPR001177; Papillom_E1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cottontail rabbit papillomavirus.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      524; E1_N; 1.
602 AA; 68015 MW; 8458F4C93DA1F64B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
EMBL: AE003646: AAF53440.1: -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          602 AA.
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6; Mismatches
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SMART; SM00355; ZBC_CZH2; 8.
PROSITE; PS00028; ZINC_FINGER_CZH2_1; 7.
PROSITE; PS50157; ZINC_FINGER_CZH2_2; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42;
Pred. No.
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
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NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ404003; CAB96164.1; -.
InterPro: IPR001177; Papillom_E1.
Pfam; PF00519; E1; 1.
                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00519; E1: 1. Pfam: PF00524; E1_N: 1. SEQUENCE 602 AA; 67904 MW; A9B3382E4533CACB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23CC61B4B296E948 CRC64;
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                                                              Last sequence update)
Last annotation update)
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602 AA
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Matches 8; Conservative
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6 VVKKXYSFKPMPLXR 20 || || |: ||:|| | 231 VVSDKYNLKPIPLKR 245 <u>ئ</u> و

Search completed: February 27, 2002, 11:50:07 Job time: 986 sec

12, Appl 12, Appl 12, Appl 3, Appli 4, Appli 73, Appli 74, Appli

Sequence

Sequence Seq

Title: Perfect score:

Run on:

Scoring table: Sequence:

Searched:

Minimum DB seq Maximum DB seq

Database

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Van Oostrum, Jan
APPLICANT: Galakatos, William C.
APPLICANT: Galakatos, Nicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: Van Heeke, Gino
TITLE OF INVENTION: CSA Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5807824Agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
STATE: NJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.5%; Score 47; DB 1; Length 74; 100.0%; Pred. No. 0.35;
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APPLICATION NUMBER: US/08/463,224
                                       US-08-557-210A-5
US-08-912-129A-58
US-08-912-129A-44
US-08-912-129A-54
US-08-912-129A-50
US-08-912-129A-50
US-08-912-129A-51
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US-08-912-129A-61
US-08-912-129A-61
US-08-91-125A-4
US-08-91-175A-4
US-08-781-891-73
US-08-781-891-74
US-08-781-891-74
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0, Mismatches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ATORNEY/AGENT INFORMATION:
NAME: FOLCY, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
TELEFAX: 908-654-7866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08463224 Patent No. 5807824
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 74 amino acids
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YerulE TYPE: protein
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Sequence 24, Appl
Sequence 7, Appli
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3.405 Million cell updates/sec
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                                                                                                                                                                           February 27, 2002, 11:36:03; Search time 132.19 Seconds
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. /cgn2_6/ptodata2/liaa/5B_COMB.pep:*
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. /cgn2_6/ptodata2/liaa/PCTUS.COMB.pep:*
. /cgn2_6/ptodata3/liaa/PCTUS.COMB.pep:*
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-246-5008-10
US-09-246-5008-14
US-08-299-285-7
US-08-299-285-7
US-08-995-126-7
US-08-995-126-7
CS-08-995-126-7
PCT-US95-11126-7
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US-08-299-285-13
US-08-985-126-5
US-08-955-126-13
PCT-US95-11126-13
PCT-US95-11126-13
US-08-299-285-14
US-08-299-285-14
US-08-299-285-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-985-126-23
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                                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                              1 KYKHSVVKKXYSFKPMPLXR 20
                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                 US-09-446-109A-6
..99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length DB
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Score

Result . 9 ö

Gaps

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Gaps

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APPLICANT: Hugli, Tony E.

TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
TITLE OF INVENTION: Substrates
TITLE OF INVENTION: Using the Substrates
FILE REFERENCE: 24730-220
CURRENT APPLICATION NUMBER: US/09/246,500B
CURRENT FILING DATE: 1999-02-08
NUMBER OF SEO ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sherman, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Sherman, TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Sulte 720
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.5%; Score 47; DB 4; Length 77; 100.0%; Pred. No. 0.36; ive 0; Mismatches 0; Indels
                                                                                                                         Score 47; DB 4; Length 74;
Pred. No. 0.35;
                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-OOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: US/08/299,285
31-AUG-1994
                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/09246500B Patent No. 6235494
) ORCANISM: Human C5a Anaphylatoxin; FEATURE: NAME/KEY: CARBOHYD: LOCATION: (64)...(66)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mouse C5a Anaphylatoxin
US-09-246-500B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08299285 Patent No. 5696230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                           47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                           Query Match 47.5
Best Local Similarity 100.
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19103-2307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                    12 KYKHSVVKK 20
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Hugli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KYKHSVVKK 9
                                                                                                                                                                                                 1 KYKHSVVKK 9
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                                                                                                                                                                                                                                                                                                       US-09-246-500B-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-299-285-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                            APPLICANT: van Oostrum, Jan
APPLICANT: Boyar, William C.
APPLICANT: Bolakatos, Wicholas G.
APPLICANT: Schmitz, Albert
APPLICANT: van Heeke, Gino
TITLE OF INVENTION: C5a Receptor Antagonists Having
TITLE OF INVENTION: Substantially No. 5837499Agonist Activity
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lerner, David, Littenberg, Krumholz & Mentlik
STREET: 600 South Avenue West
CITY: Westfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: CALLOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
0.35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.5%; Scc.
100.0%; Pre
0;
                                                                                        ; Sequence 3, Application US/08463377
; Patent No. 5837499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: FOLEY, Shawn P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 139-125
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 74 amino acids
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Best Local Similarity 100...
... 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 900-000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linear
                                                                                                                               GENERAL INFORMATION:
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     12 KYKHSVVKK 20
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                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-463-377-3
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APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor's Yeephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 10;
                                                                                                                                                                           Score 42; DB 1; Length 10;
Pred. No. 0.32;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: "D-Alanine at position 9" US-08-299-285-24
                                                       NAME/KEY: Modifled-site
LOCATION: 9
COTHER INFORMATION: "D-Alanine at position 9"
US-08-299-285-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.4%; Score 42; DB 1;
80.0%; Pred. No. 0.32;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/08299285 Patent No. 5696230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ret., Janet E.
REGIETATATON UNBER: 36,252
REFERENCE/DOCKET NUMBER: 6307;
TELECOMMUNICATION INFORMATION:
TELEPONS: 7151563-4100
TELEFAX: 7) 563-404
INFORMATION FOR SEQ 75 NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SS: not relevant not relevant
                                                                                                                                                                                  42.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 31-AUG-1994
CLASSIFICATION: 530
ATTORNEY/ACEVIT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site LOCATION: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: C-terminal
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE C: SecrERISTICS: LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                  Query Match 42.4
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       US-08-299-285-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
WUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTR: CASTELL FOR COUNTRY US
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/299,285
FILING DATE: 31-AUG-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
RECISTATION NUMBER: 36,252
RECISTATION NUMBER: 36,252
FELECOMMUNICATION NUMBER: 36,252
FELECOMMUNICATION NUMBER: 36,254
TELEFRAX: (215) 563-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42; DB 1
Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                         ; Sequence 10, Application US/08299285
; Patent No. 5696230
                                                                                                                                                                                                                             TOPOLOGY: not relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    42.4%;
80.0%;
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
TOPOLOGY: not relevant
LECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match . 42.4
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 YSFKPMPLXR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
US-08-299-285-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-08-299-285-10
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APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 2;
Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: "D-Alanine at position US-08-985-126-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION:
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER:
11 NG DATE:
TILING DATE:
TILING DATE:
TILING DATE:
TOTALNG DATE:
TOTALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: No. 5942599 Relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24, Application US/08985126
Patent No. 5942599
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.4%;
80.0%;
                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity Bu.v.
Best Local Similarity Bu.v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YSFKDMPLAR 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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                                                                                                                                                                                                                                                                                                                             APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/985,126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 2;
Pred. No. 0.32;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
ATTORNEV,AGENT INFORMATION:
NAME: Reed, Janet E.
RECISTRATION NUMBER: 36,252
RECISTRATION NUMBER: 36,252
RECISTRATION NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4004
: TELEPHONE: (215) 563-4044
: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: No. 5942599 Relevant
TOPOLOGY: No. 594259 Relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
                                                                                                                                                                                                                                  ; Sequence 7, Application US/08985126
; Patent No. 5942599
; GENERAL INFORMATION:
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Best Local Similarity 80.u
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                                                        11 YSFKPMPLXR 20
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HYPOTHETICAL:
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; FRAGMENT TYPE:
US-08-985-126-7
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                                                                                                                                                                                                         US-08-985-126-7
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APPLICANT: Sanderson, Sam D.
APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonid
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/11126
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0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application PC/TUS9511126 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
                                                                                                                                             NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFRENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-404
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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INFORMATION FOR SHU ID NO: 1
SEQUENCE CHARACTERISTICS:
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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CLASSIFICATION:
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FRAGMENT TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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APPLICANT: Sherman, Simon A.
APPLICANT: Sherman, Simon A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
WUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42; DB 2; Length 10;
Pred. No. 0.32;
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STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,126
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; OTHER INFORMATION: "D-Alanine at position 9"
US-08-985-126-24
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                                                                                                                                                                                                                                                                                                                    CLASSIFLATION:
PRIOR APPLICATION NUMBER: US/08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: REEd. Janet E.
REGISTRATION NUMBER: 36,252
REGISTRATION NUMBER: 36,252
RECENENCE/DOCKET NUMBER: 63075
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: No. 5942599 Relevant
TOPOLOGY: No. 594259 Relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/11126
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ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DO
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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                          19103-2307
                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                   FILING DATE:
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COUNTRY:
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APPLICANT: Sherman, Simon A.
APPLICANT: Kirnarsky, Leonin A.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
ADDRESSEE: Dann, Dorfman, Herrell and Skillman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 1; Length 10; Pred. No. 0.47;
: LOCATION: 9
; OTHER INFORMATION: /product- "D-Alanine at position 9"
PCT-US95-11126-24
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                                                                                                         Length 10;
                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADTRESSE: Daily, DUINMAIN, MELTELL AND STITING STATE: Philadelphia STATE: Philadelphia STATE: Philadelphia STATE: PA COUNTY: US 21P: 19103-2307 COMPUTER READABLE FORM: MEDTUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/299,285 FLING DATE: 31-AMG-1994 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: Reed, Janet E. REGISTRATION NUMBER: 63075 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Dann, Dorfman, Herrell and Skillman
1601 Market Street Suite 720
                                                                                                         Score 42; DB 5;
Pred. No. 0.32;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08299285 Patent No. 5696230 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS: not relevant not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-404
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.48;
80.08;
                                                                                                           42.4%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 amino acids
                                                                                       Query Match
Best Local Similarity 80.0،
المالية Similarity 80.0،
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 YSFKPMPLXR 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FRAGMENT TYPE:
US-08-299-285-5
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US-08-299-285-13
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                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sanderson, Sam D.
APPLICANT: Sharman, Simon A.
APPLICANT: Therann, Simon A.
APPLICANT: Taylor, Stephen M.
APPLICANT: Taylor, Stephen M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: C-Terminal Analogs of C5a Anaphylatoxin
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C.
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                  Score 42; DB 5; Length 10;
Pred. No. 0.32;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSILLANTON.
PRIOR APPLICATION NUMBER: US 08/299,285
FILING DATE: 31-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: 63075
TELEPHONE: (215) 563-4100
TELEPHONE: (215) 563-4044
INFORMATION FOR SEO ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application PC/TUS9511126 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZUP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
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not relevant
                                                                                                                                                                                                                                                                                                     42.48;
80.08;
                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
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                                                                                                                                                 C-terminal
              10 amino acids
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Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                      11 YSFKPMPLXR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                         HYPOTHETICAL: N
ANTI-SENSE: NO
FRAGMENT TYPE:
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              LENGTH:
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GENERAL INFORMATION:
APPLICANT: Sanderson, Sam D.
APPLICANT: Shandard. Simon A.
APPLICANT: Sheman, Simon A.
APPLICANT: Sheman, Simon A.
APPLICANT: Taylor, Stephon M.
TITLE OF INVENTION: High Affinity Response-Selective
TITLE OF INVENTION: CTerminal Analogs of C5a Anaphylatoxin
NUMBER OF SOUGHES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE Dann, Dorfman, Herrell and Skillman
STREET, 1601 Market Street Suite 720
COUNTRY: PAL CAPPORT OF COMPALIANE
STATE: PA
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BW PC Compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: 36,252
RECISTRATION NUMBER: 36,252
REFERENCE/DOCKET INFORMATION:
NAME: Reed, Janet E.
RECISTRATION NUMBER: 36,33-4100
TELEPHONE: (215) 563-4404
TELEPHONE: (215) 563-4404
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid
STRANDEDMESS: NO
ANTICATION: TREEVANT
MODEULE TYPE: PEPTING
MAIN CANTON: TREEVANT
MODEULE TYPE: PEPTING
MAIN CANTON: OC TELEVANT
MODEULE TYPE: PEPTING
MAIN CANTON: ANTI-SENSE: NO
PRAMINE: NO
PRAMINE: C-CLEMINAL
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COCATION: 9
OTHER INFORMATION: "D-Phenylalanine at
US-08-299-285-13
Sequence 13, Application US/08299285 Patent No. 5696230 GENERAL INFORMATION:
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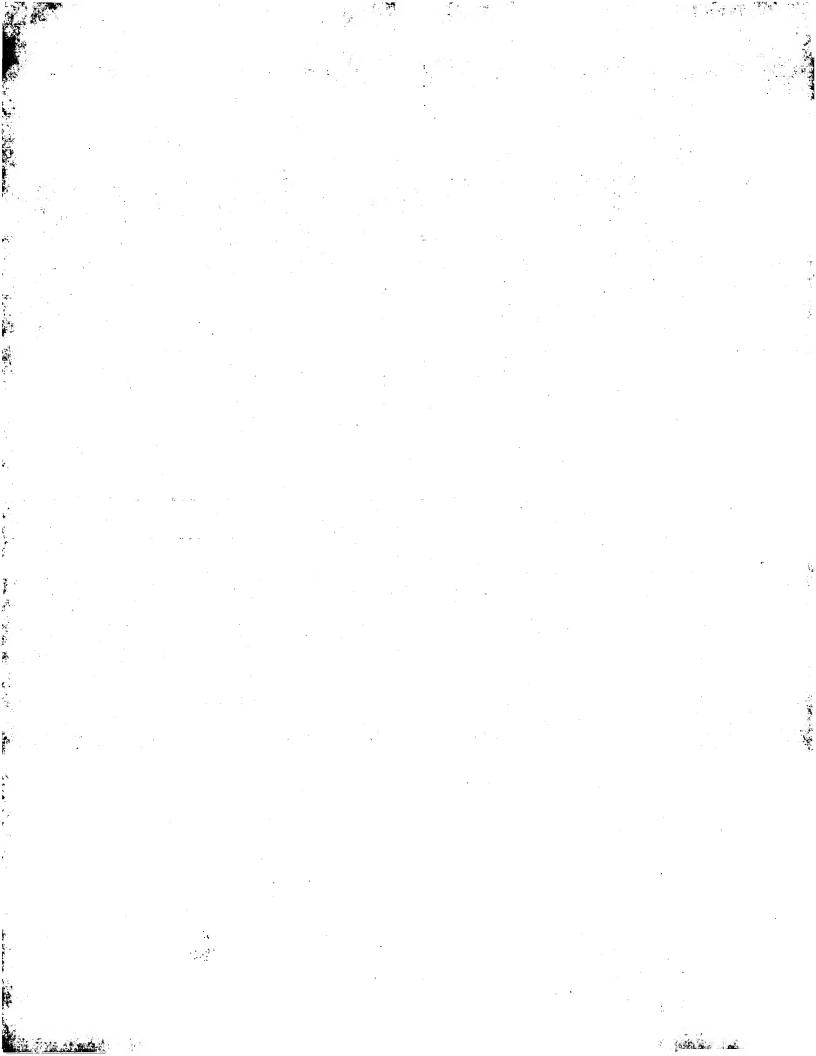
Gaps .; 0 41.4%; Score 41; DB 1; Length 10; 80.0%; Pred. No. 0.47; Live 0; Mismatches 2; Indels 2; Indels Ouery Match
Best Local Similarity 80.0
Matches 8; Conservative

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11 YSFKPMPLXR 20 g ò

1 YSFKDMPLFR 10

Search completed: February 27, 2002, 11:36:03 Job time: 142 sec



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Anaphylatoxin; receptor; ligand; antiinflammatory; hexapeptide; heptapeptide; immunodeficiency; allergy; autoimmune; ARDS; cancer; infection; endotoxin; asthma; gout; psoriasis; cirrhosis; inflammatory; bowel; disease; hepatitis; burns; myocardial; infarction; transplant rejection; ischaemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anaphylatoxin antagonist or agonist peptide.
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AAR30577
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/ SIDS8/gcgdata/geneseq/geneseqp/AA1990_DAT:
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/ SIDS8/gcgdata/geneseq/geneseqp/AA1991_DAT:
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		Anaphylacoxin anta	C5a peptide analog	Human D2H binding	Corn putative ledi	E. coli growth and	Yeast G protein-co	Yeast G protein-co	Yeast G protein.co	Yeast G protein-co	Yeast G protein-co	Yeast G protein-co
	ID		AAR303//	AAR89737	AAW74031	AAB01208	AAG98875	AAY58359	AAY58360	AAY58358	AAY58356	AAY58357	AAY58355
	98	::	7	16	20	21	22	21	21	21	21	21	21
	Duery Match Length DB	:	٥	9	39	434	462	700	847	864	953	953	961
æ	Query		7.6	94.3	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7
	Score		า	33	30	30	30	30	30	30	30	30	30
	Result No.		-	7	٣	ಶ	r	9	7	æ	6	10	11

/note= "(2R)-2-amino-3-cyclohexyl-propanoyl"

/label= OTHER

/note= "D-Arg"

Modified-site

W09211858-A 23-JUL-1992 90US-0634641.

27-DEC-1990;

10-DEC-1991;

Location/Qualifiers /note= "N-Me-Phe"

> Modified-site Modified-site

Synthetic

(first entry)

Human myotonic dys	Human colon cancer		Amino acid permeas					Q.	Amino acid sequenc	Amino acid sequenc	Amino acid sequenc	Human C5a receptor	ĽĽ	Peptide #8203 enco		Ø		Peptide #3260 enco	£	#3220	S		-deoxy-D	protein	s protein	x ORF238	mays protein	Zea mays protein f	Anti-adipocyte mon	bι	Arabidopsis thalia		
AAR41001	AAB53989	AAB93531	AAB72313	AAB67331	AAY24555	AAW66370	AAW66371	AAW66377	AAY91816	AAY91853	AAY91854	AAR64890	AAR37902	AAM21769	AAM38093	AAG56373	AAG60383	AAM16826	AAM29310	AAM04538	AAB63599	AAG19056	AAB01365	AAG40669	AAG27126	AAB40474		AAG26045	AAU02545	AAG03617	AAG10416	AAC40668	ALIGNMENTS
14																																	
1093	000	217	462	745	13	13	13	13	13	13	13	18	19	54	54	65	9	71	71	71	82	90	94	107	108	111	117	120	120	126	128	128	
85.7		82.9																															
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Claim 2; Page 54; 294pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-009568/01
                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                     1 FKPXWR 6
                              Konteatis 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-1997;
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Omahony DJ,
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| fkpxwr
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                                                                                                                                                                                                                                                                                                                                                                               AAW74031;
                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                  Matches
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  δ
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                                                                                                                          The peptide is a specifically claimed example of a group of highly generic hexa- and heptapeptides which are (a) anaphylatoxin antagonists useful for tracting asthma, other allergies, inflammations, autoimmune diseases, serum sickness, gout, bullous skin diseases, psoriasis, RRDS, endotoxin shock, hepatic cirrhosis, pancreatitis, inflammatory bowel disease, burns, sepsis, myocardial infaction, chronic hepatitis, transplant rejection, or ischaemic heart or brain damage; or (b) anaphylatoxin agonists useful for stimulating inflammatory and immune responses, e.g. in the treatment of cancer, immunodeficiency diseases and severe infections.
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSa; complement; agonist; antagonist; peptide; binding assay; identification; inflammation; pain reduction; respiratory disorder; cardiovascular; hypertension; ARDS; anaphylaxis; arthritis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "OTHER = the Bolton-Hunter modified peptide having the 3 (p-hydroxyphenyl) propionyl
                                                                    New hexa- and hepta:peptide(s) are anaphylatoxin antagonists and agonists - for treating inflammatory and immunodeficiency diseases, cancers and severe infections
                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C5a peptide analogue, C089, used to identify C5a (ant)agonists
                                                                                                                                                                                                                                                                           Length 6;
                                                                                                                                                                                                                                                                                              Indels
                            Or YS, Wagner R, Wiedeman PE;
                                                                                                                                                                                                                                                                                     4.3e+05;
                                                                                                                                                                                                                                                                         94.3%; Score 33; DB 13;
100.0%; Pred. No. 4.3e+05
iive 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "D-cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                           Claim 11; Page 153; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- Phe, OTHER
                                                                                                                                                                                                                                                                                                                                                                                      AAR89737 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- OTHER
        (ABBO ) ABBOTT LABORATORIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0215137
                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                WPI; 1992-268383/32
                            Luly JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 4
                                                                                                                                                                                                                                             6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                  1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-1994;
                                                                                                                                                                                                                                                                                                                             W09525957-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      competitive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                            AAR89737;
                                                                                                                                                                                                                                             Sequence
                            Kawai M,
                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                              AAR89737
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                                                                                                                                                                                                                                                                                                                                                                                   C5a C-terminal peptide analogues AAR89734-44 and AAR90033-35 may be u in a mew method for identifying C5a agonists/Antagonists. AAR89734 represents the generic formula of this newly defined class of labelled peptides. C5a antagonists identified using this method are useful in the treatment of a wide variety of C5a-mediated diseases such as acute respiratory distress syndrome (ARDS), anaphylactic shock, psoriasis, osteoarthritis, rheumatoid arthritis, asthma, cardiovascular disorders, and metastatic spread of cancerous tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or
                                                                                                                                                                                                            CSa receptor binding assays - used for identifying cpds.having CSa antagonist, agonist or partial agonist activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimaeras and antibodies, used to deliver therapeutic or diagnostic agents to, through, the gastrointestinal tract, e.g. insulin or leuprolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.3%; Score 33; DB 16; Length 6; 100.0%; Pred. No. 4.3e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carter JM,
J;
                                                                          Springer MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cagney GM,
, Singleton
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW74031 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                                                       Claim 15; Page 47; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human D2H binding protein DAB3.
                                                                          Siciliano SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0046595
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Patterson CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
(MERI ) MERCK & CO INC
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This sequence represents a perture that specifically to at least one of the gastro-intestinal (GI) that bind specifically to at least one of the gastro-intestinal (GI) tract receptors human intestinal peptide-associated transporter (HPTI), hereTI, D2H and human sucrose-isomaltase complex (hSI). (I) provide active transport of therapeutic agents through human and animal GI tissue (into the blood) for in vivo delivery, particularly for treatment or prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia, cancer, migraine, or angina pectoris. Specifically they are used to deliver insulin or leuprolide, but many other suitable therapeutic agents are disclosed, including genes or inhibitory nucleic acid, imaging agents and antigens. (I) may also provide targeting to the GI tract. Other uses of (I) are: (I) to determine the level of specified receptors in a sample (in a binding assay): and (ii) to screen for molecules that bind (I).

Immunogenic analogues or derivatives of (I) are used to raise antibodies and in immunoassays. The antibodies are used to locate, detect and measure (I), e.g. for imaging, monitoring treatment, tissue analysis etc., also for peptide purification and immobilisation.
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                  This sequence represents a peptide that specifically binds to the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corn: lecithin:cholesterol acyltransferase; phytosterol; phosphatidylcholine-sterol O-acyltransferase; heat shock; cold shock.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening CDNA expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide encoding plant lecithin:cholesterol acyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saylor JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
O
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Pred. No. 18;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corn putative lecithin:cholesterol acyltransferase #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shen JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 10; Page 40-41; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB01208 standard; Protein; 434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sakai H,
                                                                                                                                                                                                                                                                                                                                                                                                                                               85.7%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 66.7
les 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cahoon RE, Kinney AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-412337/35
                                                                                                                                                                                                                                                                                                                                                                                       39 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAA49203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200032791-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 frpgwr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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The gene and protein can be used to produce transgenic plants which have increased lipid metabolism and membrane fluidity, and therefore increased resistance to heat and/or cold shock, to alter the content of phytosterol or lecithin in grains and to identify potential herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH84373 to AAH84499 represent Escherichia coli growth and proliferation related DNA sequences (I). AAH84500 to AAH8670 encode the E. coli growth and proliferation related proteins given in AAG99078 and AAG9839 to AAG98999. (I) can be used as potential targets for the generation of new antimicrobial agents, and for identification of compounds which interact with the gene products of (I). In addition the expression of (I) and the purification of the proteins, the purified proteins can be used to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds. In addition, nucleic acid probes complementary to (I) that are specific for particular species of microorganisms can be used to identify particular microorganism species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. coli growth and proliferation related protein sequence SEQ ID NO:345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in clinical specimens, therefore, providing a rapid and dependable method by which to identify the causative agents of a bacterial infection. Also, antibodies generated against proteins translated from mRNA transcribed from proliferation required sequences can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids that inhibit Escherichia coli proliferation, useful for screening for homologous genes and for designing expression vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to screen for specific microorganisms that produce such proteins in a species-specific manner. AAHB4371 and AAHB4670 represent sequencing primers used in the isolation of E. coli growth and proliferation related sequence, which are used in an example from the present
                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli; growth; proliferation; microbial; antimicrobial;
                                                                                                                                                                                                ö
                                                                                                                                                             Length 434;
                                                                                                                                                                                                  1; Indels
                                                                                                                                                       Score 30; DB 21;
Pred. No. 2.1e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 19; Page 421-422; 522pp; English.
                                                                                                                                                                                                                                                                                                                                                                            AAG98875 standard; Protein; 462 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacterial infection; microorganism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohlsen K, Zyskind J;
                                                                                                                                                           85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                  Conservative
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N-PSDB; AAH84546.
                                                                                                                                                             Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                                                      434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                                                271 frpmwr 276
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                                                                                                                                                                                                                                         1 FKPXWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-MAY-200
                                                                                                                                                                                                                                                                                                                                                                                                                     AAG98875;
                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                            AAG98875
                                                                                                                                                                                                                                                                                                                                       RESULT
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      888888
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700 AA;

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Sequence
                                           Query Match
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                                                                                                                                                                                                                The invention relates to a novel yeast G protein-coupled receptor,

C GPR1 (AAY58355). GPR1 is predicted to have seven transmembrane domains,

which is characteristic of G protein-coupled receptors, and also

contains a very large third cytoplasmic loop and a large cytoplasmic

sequence (RKRAQIO) is present at the N-terminal end of the loop and the

other sequence (KKRRAQIO) is at the C-terminal end of the loop and the

third cytoplasmic loop also contains an asparagine-rich region. GPR1 is

believed to provide the upstream signal that activates GPA2, and plays

an essential role in inducing the switch from non-filamentous to

filamentous growth in yeast. Modulators of GPR1 function, especially

inhibitors, are useful for prevention or treatment of a disease or

c disorder involving a fungal infection. The inhibitor may be an anti-GPR1

antibody, GPR1 antisense nucleic acid or a GPR1 gene altered so that an

contains a very large that the contains and integral acid or a GPR1 gene altered so that an

contains a very large that acid or a GPR1 gene altered so that an

contains a very large that acid or a GPR1 gene altered so that an antised the contains and a GPR1 gene altered so that an ancidence in activate the biological activity of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Invention. This sequence is lacking the majority of the cytoplasmic C-terminal tall, relative to the native GPRI.
Note: This sequence is not shown in the specification, but is derived from the yeast GPRI amino acid sequence given in figure 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GPRI. Compounds which modulate GPRI gene expression and/or gene product activity may be used to inhibit the conversion of a fungus from a non-filamentous form to a filamentous form. The present sequence represents a GPR mutant, d277-284, used in an exemplification of
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                      Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mutein.
                                                                                                 .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel protein, gene, antibody and recombinant cell useful for identifying modulators and inhibitors useful as anti-fungals
                                                                       Length 462;
                                                       Score 30; DB 22; Length 40. Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                            Yeast G protein-coupled receptor GPR1 mutant d694-954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6.2.5; Page -; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOUN ) MOUNT SINAI SCHOOL MEDICINE
                                                                                                                                                                                                                         AAY58359 standard; Protein; 700 AA.
                                                                    Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0088311.
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                                                                                                                                                                                                                                                                               27-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-086980/07
                           462 AA;
                                                                                                                                          :11 11
398 ykplwr 403
                                                                                                                          1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                          WO9963094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirsch JP,
                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
  invention
                                                                                                                                                                                                                                                     AAY58359;
                             Sequence
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The invention relates to a novel yeast G protein-coupled receptor,

GPRI (AAY$855). GPRI is predicted to have seven transmembrane domains,
which is characteristic of G protein-coupled receptors, and also
contains a very large third cytoplasmic loop and a large cytoplasmic
sequence (KRRAQIO) is present at the N-terminal end of the loop and the
cytoplasmic loop also contains an asparagine-rich region. GPRI is
believed to provide the upstream signal that activates GPA2, and plays
an essential role in inducing the switch from non-filamentous to provide the waster and activates GPA2, and plays
an essential role in inducing the switch from non-filamentous to filamentous growth in yeast. Modulators of GPRI function, especially
inhibitors, are useful for prevention or treatment of a disease or
continody, GPRI antisense nucleic acid or a GPRI gene altered so that an
inserted heterologous sequence inactivates the biological activity of
confilamentous form to a filamentous form. The present sequence
confilamentous form to a filamentous form. The present sequence
crepresents a GPR mutant, 4377-284, used in an exemplification of
the invention. This sequence is lacking a portion (designated the
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                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protein, gene, antibody and recombinant cell useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 identifying "odulators and inhibitors useful as anti-fungals
   Length 700;
                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast G protein-coupled receptor GPR1 mutant d841-954.
Score 30; DB 21;
Pred. No. 3.5e+02;
; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6.2.5; Page -; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                     AAY58360 standard; Protein; 847 AA.
   85.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                       Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-086980/07
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                                                                                                                                                                                                        156 fkpnwk 161
                                                                                                                                           1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            native GPR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-DEC-1999
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying modulators and inhibitors useful as anti-fungals
Score 30; DB 21; Length 847;
Pred. No. 4.2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast G protein-coupled receptor GPR1 mutant d490-586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 6.2.5; Page -; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                                                                                    AAY58358 standard; Protein; 864 AA.
   85.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0088311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2000 (first entry)
                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-086980/07
   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                156 fkpnwk 161
                                                                                                                        1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1998;
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IID AAY58

AAC AAY51

XXX AAY51

XXX AAY51

XXX AAY51

XXX AAY51

XXX BBCC

SSTCC

SSTCC

SSTCC

SSTCC

XXX AAY50

SSTCC

SST
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The Invention relates to a novel yeast G protein-coupled receptor, GPRI (AAY58355). GPRI is predicted to have seven transmembrane domains, which is characteristic of G protein-coupled receptors, and also contains a very large third cytoplasmic loop and a large cytoplasmic tall. The third cytoplasmic loop contains two short basic sequences; one sequence (KRKRAQIG) is present at the N-terminal end of the loop and the other sequence (KKRRAQIO) is at the C-terminal end of the loop and the third cytoplasmic loop also contains an asparagine-rich region. GPRI is believed to provide the upstream signal that activates GPA2, and plays an essential role in inducing the switch from non-filamentous to filamentous growth in yeast. Modulators of GPRI function, especially inhibitors, are useful for prevention or treatment of a disease or disorder involving a fungal infection. The inhibitor may be an anti-GPRI antisense nucleic acid or a GPRI gene altered so that an inserted heterologous sequence inactivates the biological activity of GPRI. Compounds which modulate GPRI gene expression and/or gene product activity may be used to inhibit the conversion of a fungus from a Note: This sequence is not shown in the specification, but is derived from the yeast GPR1 amino acid sequence given in figure 1A. non-filamentous form to a filamentous form. The present sequence represents a GPR mutant, d277-284, used in an exemplification of the invention. This sequence is lacking the asparagine-rich region of the third cytoplasmic loop, relative to the native GPR1. 864 AA; Sequence Note:

Length 953;

Score 30; DB 21; Pred. No. 4.7e+02;

85.7%;

Query Match Best Local Similarity

The invention relates to a novel yeast G protein-coupled receptor, CPRI (AAY5835). GPRI is predicted to have seven transmembrane domains, which is characteristic of G protein-coupled receptors, and also contains a very large third cytoplasmic loop and a large cytoplasmic contains a very large third cytoplasmic loop and a large cytoplasmic contains two short basic sequences; one sequence (KRKRAQIG) is present at the N-terminal end of the loop and the cother sequence (KRRRAQIG) is at the C-terminal end of the loop. The third cytoplasmic loop also contains an asparagine-rich region. GPRI is believed to provide the upstream signal that activates GPAZ, and plays an essential role in inducing the switch from non-filamentous to filamentous growth in yeast. Modilators of GPRI function, especially inhibitors, are useful for prevention or treatment of a disease or disorder involving a fungal infection. The inhibitor may be an anti-GPRI antibody, GPRI antisense nucleic acid or a GPRI gene altered so that an inserted heterologous sequence inactivates the biological activity of activity may be used to inhibit the conversion of a fungus from a non-filamentous form to a filamentous form. The present sequence conversion of a fungus from a non-filamentous form to a filamentous form. The present sequence is lacking the first basic motif (KRIKAQIG) of the third cytoplasmic loop, realative to the native GPRI.

Note: This sequence is not shown in the specification, but is derived from the yeast GPRI amino acid sequence given in figure 1A. ö Gaps Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mutein. ö identifying modulators and inhibitors useful as anti-fungals Score 30; DB 21; Length 864; Pred. No. 4.3e+02; 1; Mismatches 1; Indels Novel protein, gene, antibody and recombinant cell useful least G protein-coupled receptor GPR1 mutant d277-284. Example 6.2.5; Page -; 63pp; English. (MOUN) MOUNT SINAI SCHOOL MEDICINE. AAY58356 standard; Protein; 953 AA. 85.7%; 66.7%; 98US-0088311 99WO-US11838 (first entry) 4; Conservative Saccharomyces cerevisiae WPI; 2000-086980/07 Query Match Best Local Similarity dirsch JP, Xue Y; 953 AA; ||| |: |56 fkpnwk 161 1 FKPXWR 6 27-MAR-2000 409963094-A2 28-MAY-1999; 01-JUN-1998; Sequence Synthetic AAY58356; Matches AAY58356 RESULT ဖ

1 FKPXWR 6

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The invention relates to a novel yeast G protein-coupled receptor,

C GPR1 (AAY58355). GPR1 is predicted to have seven transmembrane domains,

Which is characteristic of G protein-coupled receptors, and also

contains a very large third cytoplasmic loop and a large cytoplasmic

tail. The third cytoplasmic loop contains two short basic sequences; one

sequence (KKRRAQIO) is present at the N-terminal end of the loop and the

cytoplasmic loop also contains an asparagine-rich region. GPR1 is

chird cytoplasmic loop also contains an asparagine-rich region. GPR1 is

believed to provide the upstream signal that activates GPR2, and plays

an essential role in Inducting the switch from non-filamentous to

filamentous growth in yeast. Modulators of GPR1 function, especially

inhibitors, are useful for prevention or treatment of a disease or

disorder involving a fungal infection. The inhibitor may be an anti-GPR1

chaptody, GPR1 antisense nucleic acid or a GPR1 gene altered so that an

inserted heterologous sequence inactivates the biological activity of

GPR1. Compounds which modulate GPR1 gene expression and/or gene product

cactivity may be used to inhibit the conversion of a fungus from a

non-filamentous form to a filamentous form. The present sequence

crepresents a GPR mutant, d610-617, used in an exemplification of

the invention. This sequence is lacking the second basic modif

(KKRRAQIO) of the third cytoplasmic loop, relative to the native GPR1.

C from the yeast GPR1 amino acid sequence given in figure 1A.
   ö
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mutein.
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   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yeast G protein-coupled receptor GPR1 mutant d610-617.
   ä
   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOUN ) MOUNT SINAI SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                       AAY58357 standard; Protein; 953 AA.
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae.
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         953 AA;
                                                                                                                                 156 fkpnwk 161
                                                             1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                           AAY58357;
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                                                                                                                                                                                                                                         RESULT 10
   Matches
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AAY 58
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Yeast, G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form: signalling pathway; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Basic motif 2 (KKRRAQIQ)"
                                                                                                                                                                                                                                                                                                                                                                              "Basic motif 1 (KRIKAQIG)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note* "Intracellular C-terminus"
                                                                                                                                                                      /note= "Extracellular N-terminus"
                                                                                                                                                                                                                                                                                                                                                                                                                       .645
ce= "Transmembrane domain 6"
                                                                                                                                                                               56 .80
/note= "Transmembrane domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                "Asparagine-rich region"
                                                                                                                                                                                                                                                          "Transmembrane domain 3"
                                                                                                                                                                                                                                                                                  181..200
/note= "Transmembrane domain 4"
                                                                                                                                                                                                                         "Transmembrane domain 2"
                                                                                                                                                                                                                                                                                                                            /note≈ "Transmembrane domain 5"
                                                                                                                                                                                                                                 116..132
/note= "Extracellular loop 1"
                                                                                                                                                                                                                                                                                                   201..246
/note= "Extracellular loop 2"
247..276
                                                                                                                                                                                                                                                                                                                                                    ..620
te= "Intracellular loop 3"
                                                                                                                                                                                                                                                                          "Intracellular loop 2"
                                                                                                                                                                                                        "Intracellular loop 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Extracellular loop 3"
                                                                                                                                                                                                                                                                                                                                             'note= "Encoded by AGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Encoded by AGC"
                                                                                            Yeast G protein-coupled receptor GPR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                     Location/Qualifiers
                                          AAY58355 standard; Protein; 961 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0088311.
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                                                                           (first entry)
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277..284
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646..656
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                                                                                                                                     Saccharomyces cerevisiae
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                                                                                                                                                                                                         /note-
                                                                                                                                                                                                                                                            'note-
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                                                                                                                                                                                                                                                                                                                                     Misc-difference 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lisc-difference 250
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156 fkpnwk 161
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                                                                          27-MAR-2000
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                                                          AAY58355;
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Gaps

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This sequence represents a novel yeast G protein-coupled receptor,
GPR1. GPR1 is predicted to have seven transmembrane domains.
which is characteristic of G protein-coupled receptors, and also
contains a very large third cytoplasmic loop and a large cytoplasmic
sequence (KRIKAOIG) is present at the N-terminal end of the loop and the
other sequence (KRIRAOIG) is at the C-terminal end of the loop and the
other sequence (KRIRAOIG) is at the C-terminal end of the loop and the
other sequence (KRIRAOIG) is at the C-terminal end of the loop and the
cother sequence (KRIRAOIG) is at the C-terminal end of the loop and the
cother sequence (KRIRAOIG) is at the San asparagine-rich region. GPR1 is
believed to provide the upstream signal that activates GPR2, and plays
an essential role in inducing the switch from non-filamentous to
filamentous growth in yeast. Modulators of GPR1 function, especially
inhibitors, are useful for prevention or treatment of a disease or
disorder involving a fungal infection. The inhibitor may be an anti-GPR1
antibody, GPR1 antisense nucleic acid or a GPR1 gene altered so that an
instruct of Compounds sequence inactivates the biological activity of
activity may be used to inhibit the conversion of a fungus from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *encoded by predicted reading frame a, x's in the sequence indicate stop codons in the reading frame"
                                                                  Novel protein, gene, antibody and recombinant cell useful for identifying modulators and inhibitors useful as anti-fungals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.7%; Score 30; DB 21; Length 961; 66.7%; Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abnormality; muscular dystrophy; CHR 19; chromosome 19; protein kinase; polymerase chain reaction; brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-filamentous form to a filamentous form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human myotonic dystrophy gene protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1..1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR41001 standard; Protein; 1093 AA
                                                                                                                  Claim 4; Fig 1A; 63pp; English.
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Matches 4; Conservative
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              WPI; 2000-086980/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 961 AA;
                             N-PSDB; AAZ55699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 fkpnwk 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR41001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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This invention describes a novel avian-paramyxovirus cDNA (I) which comprises a nucleic acid sequence corresponding to the 5' terminal end of the genome of avian-paramyxovirus allowing the generation of an infectious copy of avian-paramyxovirus. The cell line is useful for the production of infectious lentogenic NDV (Newcastle Disease virus) without the addition of exagenous proteolytic activity. Also it is obscible to generate a stable transfected cell line that expresses the wild-type F protein in the virus envelope therefore providing infectious particles, useful in the form of a vaccine, especially against respiratory and/or gastrointestinal diseases. NDV can be easily cultured to very high titers in embryonated eggs. Mass culture of embryonated eggs is relatively cheap. NDV vaccines are relatively stable and can be eggs is relatively cheap. NDV vaccines are relatively stable and can be simply administered by mass application methods e.g. drinking water or by spraying or by aerosol formation. The natural route of infection is by the respiratory and/or gastrointestinal tract which are also the major
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New avian paramyxovirus cDNA, useful for production of vaccine against
Newcastle disease virus
                                                                                                                                                                                                                                                                                                         Gaps
                                     DNA sequence of myotonic dystrophy gene - used to produce probes and identify CHR 19 abnormality and protein kinase responsible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Avian-paramyxovirus; infection; lentogenic; F protein; vaccine; respiratory disease; gastrointestinal disease; poultry pathogen;
                                                                                                                                                                                                                                                                                                       ö
                                                                                                                               The sequence is that encoded by predicted reading frame a of the human myotonic dystrophy (DM) gene. It may be used in the identification of individuals affected by DM.
                                                                                                                                                                                                                                                               Score 30; DB 14; Length 1093;
Pred. No. 5.5e+02;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newcastle disease virus LaSota genome encoded protein 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koch G, Gielkens ALJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY51233 standard; Protein; 2204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 3; 115pp; English.
                                                                                             Disclosure; Fig 6; 64pp; English.
                                                                                                                                                                                                                                                                   85.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-NL00377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98EP-0202054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              De Leeuw OS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                   Query Match 85.7
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Newcastle disease virus.
WPI; 1993-288410/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-106102/09
                                                                                                                                                                                                              Sequence 1093 AA
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382 frprwr 387
                                                                                                                                                                                                                                                                                                                                             1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY51233;
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Gaps

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us-09-446-109a-7.rag

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AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardidoactive, muscular; human colon cancer antigens can be used in gene therapy. The colon cancer antigen polynucleotides, can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, immune system disorders, muds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAC98707 represent sequences used in the exemplification of the present
                                                                                                                                                                                            ö
routes of infection of many other poultry pathogens. NDV can induce local immunity despite the presence of circulating maternal antibody. This sequence represents a protein encoded by the NDV strain LaSota genome which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; colon cancer; colon cancer antigen; diagnosis; detection; ldentification; cyostatic; cardioactive; neuroprotective; vulnerary; Immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antilinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder;
                                                                                                                                                                                            ;
                                                                                                                                                  Score 30; DB 21; Length 2204; Pred. No. 1.1e+03; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human colon cancer antigen protein sequence SEQ ID NO:1529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infectious disease; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 2083-2084; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                   AAB53989 standard; Protein; 90 AA.
                                                                                                                                                    85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0124270
                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAR-2001 (first entry)
                                                                                                                                Ouery Match
Best Local Similarity 66.7
4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-587534/55
                                                                                                2204 AA;
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                                                                                                                                                                                                                                                                    1844 frplwr 1849
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                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotide which comprises a 3' end sequence, where the obliganceleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamamoto J;
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                                                                                 21; Length 90;
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, Otsuki T;
                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID 12886; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi K, S
A, Nagai K,
                                                                               DB 67;
                                                                                                                    Mismatches
                                                                                   Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  Human protein sequence SEQ ID NO:12886.
                                                                                                                                                                                                                                                                            AAB93531 standard; Protein; 217 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isoqai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0241899.
                                                                                 82.9%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000; 2000EP-0116126.
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                     Conservative
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                                                               Query Match
Best Local Similarity
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                              90 AA;
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| 74 fkpcwk 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1074617-A2
                                                                                                                                                                                                                                                                                                                                               26-JUN-2001
                                                                                                                                                      1 FKPXWR
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invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishii S,
                                                                                                                                                                                                                                                                                                                AAB93531;
                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ota T,
                                                                                                                                                                                                                                                            AAB93531
                                                                                                                                                                                                                                           RESULT
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AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
8 \times 8 \times 8
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Sequence 217 AA;

ó, 0; Gaps Query Match 82.9%; Score 29; DB 22; Length 217; Best Local Similarity 80.0%; Pred. No. 1.7e+02; Matches 4; Conservative 0; Mismatches 1; Indels

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og o

Search completed: February 27, 2002, 11:41:15 Job time: 454 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Search time 145.23 Seconds February 27, 2002, 11:45:17; Run on:

(without alignments)
3.147 Million cell updates/sec

US-09-446-109A-7 Perfect score: Sequence:

1 FKPXWR 6

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	formate hydrogenly	hypothetical 47.4	probable femA prot	hypothetical prote	peptide transport	probable maturase	hypothetical prote	hypothetical 47.5	probable amino aci	conserved hypothet	hypothetical prote	probable membrane	G protein-coupled	genome polyprotein	hypothetical prote	yedG protein - Esc		hypothetical prote	LPS biosynthesis R	hypothetical prote	protein F2D10.28 (conserved hypothet	amino acid permeas	nodulation competi	hypothetical prote	hypothetical prote	probable glucose-6	glutamatecystein	carboxylesterase (
	. CI	C64364	E65146	H71279	B86020	T18250	S78199	н72667	E65131	B86002	B69805	T31640	S67568	JC5808	RRNZNV	T36433	H64956	F85810	T24993	н69147	H75484	C86340 ·	H82504	T15052	A59268	G72753	S77373	B82967	T05142	534607
	08	~	~	~	~	7	7	7	~	~	7	~	7	7	-	7	2	~	7	~	~	7	7	7	~	7	~	7	7	-
	Length	380	412	498	557	623	1035	239	462	462	909	684	196	962	2204	119	217	222	301	395	412	435	458	462	467	473	477	488	523	554
æ	Ouery	94.3	94.3	94.3	94.3	94.3	88.6	85.7	85.7	85.7	85.7	85.7	85.7	85.7													82.9		•	82.9
	Score	33	33	33	33	33	31	30	30	30	30	30	30	30	30	29	29	58	29	58	29	58	29	29	58	29	29	29	29	29
	Result No.	-	7	Ю	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

asparagine synthas	hypothetical prote	pumilio family pro	gene cob intron 3	_	hypothetical prote	_		hypothetical prote	hypothetical prote	envelope protein E	transposase - Myco	transposase - Flav	probable transloca	chitinase (EC 3.2.	hypothetical prote
T39308	T30044	T50143	S25952	T38755	T48944	S28301	D86400	T48945	B70438	VMWJBV	S10929	A49895	T37841	JE0183	E84788
557 2	655 2	732 2	1224 2	2685 2	84 2	162 2	174 2	195 2	227 2	233 1	254 2	254 2	273 2	275 2	297 2
				82.9		80 · C	0.08	0.08	80.0	80.0	80.0	80.0	80.0	80.0	0.08
53	29	29	29	29	28	28	28	28	28	28	28	28	28	28	28
30	31	32	33	34	35	36	37	38	5	0	1	~	13	14	51

ALIGNMENTS

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Circossion: C64364
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
R:Bult, C.J.; Woerbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Wocse
A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Wocse
A; Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
A; Accession: C64364
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1·380 < BUL>
                                                  C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
formate hydrogenlyase, subunit 5 - Methanococcus jannaschii
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A; Cross-references: GB:U67501; GB:L77117; NID:g2826289; PIDN:AAB98504.1; PID:g1591218 (; Genetics:

(; Superfamily: NADH dehydrogenase (ubiquinone) 49K protein A; Map position: REV458767-457625

Gaps ; Score 33; DB 2; Length 380; Pred. No. 27; 0; Mismatches 1; Indels 94.3%; 83.3%; Query Match 94.3 Best Local Similarity 83.3 Matches 5; Conservative

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111 11 241 FKPVWR 246 1 FKPXWR 6 ŏ Ob

Probletical 47.4 kD protein in rhsB-pit intergenic region - Escherichia coli (strain Wildernate names: hypothetical protein f409
C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C; Accession: E65146; S47710
R; Blactuner, Fx.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1452-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID: 97426617
A; Status: nucleic acid sequence not shown; translation not shown

A;Cross-references: GB:AE000425; GB:U00096; NID:q2367232; PIDN:AAC76515.1; PID:g23672 A;Experimental source: strain K-12, substrain MG1655 A; Molecule type: DNA A; Residues: 1-412 <BLAT>

R;Plunkett, G. Submitted to the EMBL Data Library, March 1994

q

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A:Molecule type: DNA
A:Residues: 1-1035 <LAN>
A:Residues: 1-1035 <LAN>
A:Cross-references: ENBL:X54421
A:Experimental source: Strain ad7-50h
R:Lang, B.F.; Ahne, F.; Bonen, L.
J. Mol. Biol. 184, 353-366, 1985
A;Title: The mitochondrial genome of the fission yeast Schizosaccharomyces pombe. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable maturase protein 3 - fission yeast (Schizosaccharomyces pombe) mitochondrion NAlternate names: gene cob intron 1 protein C:Species: mitochondrion Schizosaccharomyces pombe C;Date: 29-Jan-1998 #sequence_revision 20-Peb-1998 #text_change 21-Jul-2000 C:Accession: S78199; S10070; S67378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, August 1990
A:Description: The mitochondrial genome of the fission yeast Schizosaccharomyces pomb chizosaccharomyces pombe and Aspergillus nidulans.
A:Reference number: $78195
A:Accession: $78199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Genome: mitochondrion
A:Genome: mitochondrion
A:Genome: SCC2
C:Superfamily: cytochrome b6 homology; cytochrome b homology; plastoquinol--plastocya
C:Superfamily: cytochrome b6 homology; cytochrome b homology; plastodognio: cytochrome b exon l encoded
F:10-228/Region: cytochrome b homology #status atypical <CBH>
F:10-228/Domain: cytochrome b6 homology CAB6>
F:222-228/Domain: cytochrome b6 homology CAB6>
F:222-228/Domain: cytochrome b6 homology cAB6>
F:222-228/Domain: cytochrome b6 homology cAB6>
F:229-1035/Region: cytochrome b6 intron encoded
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide transport protein - yeast (Candida albicans)
C;Species: Candida albicans
R;Species: T18250
R;Species: T18250
A;Reference number: Z18831
A;Ref
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Pred. No. 44;
0; Mismatches 1; Indels
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              Pred. No. 40;
0; Mismatches
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A;Accession: S10070
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83.3%;
         Best Local Similarity 83.3%;
Matches 5; Conservative
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A;Residues: 1-1035 <LAW>
A;Cross-references: EMBL:X02819
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Best Local Similarity
Matches 5; Conserv
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| 445 FKPIWR 450
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A:Introns: 475/3
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                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C:Accession: H71279
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDC they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Schence 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770
A;Accession: H71279
A;Access
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B86020
B86020
C: Species: Escherichia coli
C: Species: Escherichia coli Olio IIII Coli Mayhew
Iller, L.; Grotbeck, E. J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A:Title: Genome sequence of enterchemorrhagic Escherichia coli Olio IIII
A:Title: Mayhew
A:Reference number: A85480; MUD:21074935; PMID:11206551
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A;Experimental source: strain Nichols
C;Genetics:
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A;Cross-references: GB:AE005174; NID:g12518181; PIDN:AAG58622.1; GSPDB:GN00145; UWGP:248
A:Experimental source: strain 0157:H7, substrain EDL933
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                             A.Accession: S47710
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-398, MLLSRCFAGSI' <PLU>
A.Cross-references: EMBL:U00039; NID:9466582; PIDN:AAB18466.1; PID:9466627
A.Note: this sequence has been corrected
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Pred. No. 36;
0; Mismatches
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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A; Reference number: S47666
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Best Local Similarity
Matches 5; Conserv
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A;Molecule type: DNA
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240 FKPKWR 245
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Gene: 24888
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lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Gallzzi, A.; Gallzci, A.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurlta, K.; Lapidus, A.; Lardino, A.; Authors: Lauber, J.; Lazarevic, V.; Iee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauy, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T. N.; Porlete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seaketter, W.; Winters, P.; Wipat, A.; Yamanac, T.; Tognoni, A.; Togato, V.; Uchlya, A.; Winters, P.; Wipat, A.; Yamanaco, H.; Yamane, K.; Yasunoto, M.; Reference number: A.; Reference number: Ag580; MUID:98044033
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A;Experimental source: strain 168
                                                                                                                                      K;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Rolecule type: DNA
A;Residues: 1-462 <870>
A;Cross-references: GB:AE005174; NID:g12517998; PIDN:AAG58478.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
probable amino acid/amine transport protein yhfM [imported] - Escherichia coli (strai
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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A;Molecule type: DNA
A;Residues: 1-606 <KUN>
A;Residues: 1-606 <KUN>
A;Cross-references: GB:299108; GB:AL009126; NID:g2633055; PIDN:CAB12672.1; PI
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C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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A.Reference number: A85480; WUID:21074935; PMID:11206551
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T31640
hypothetical protein Y57A10A.r - Caenorhabditis elegans
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Pred. No. 1.3e+02;
1; Mismatches 1;
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Pred. No. 1.7e+02;
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ilarity 66.7%;
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Best Local Similarity
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                                                                                                            C; Accession: B86002
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                                                                                                                                                                                                                                                                                                                                             C. Species: Aeropyrum pernix
C. Species: Aeropyrum pernix
C. Species: Aeropyrum pernix
C. Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C. Accession: H72667
R. Ravarabayası, Y. ; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takarawa, H.; Takaniya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A. Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A: Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: APE0766
C;Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTHIC
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A;Residues: 1-239 <KMbook, A;Residues: 1-239 <KMbook, NID:g5104188; PIDN:BAA79744.1; PID:g5104429
A:Experimental source: strain Kl
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       Length 1035;
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Pred. No. 1.38+02;
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Score 31; DB 2;
Pred. No. 1.8e+02;
1; Mismatches 1
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66.7%; Pred. No. 70;
iive 1; Mismatches
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          88.68;
66.78;
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nes 4; Conserv
   Query Match
Best Local Similarity
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Matches 4; Conserv
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105 FKPSWQ 110
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398 YKPLWR 403
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Best Local S
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A;Residues: 1-962 <YUN>
C;Comment: This protein monitors the extracellular signal such as nutrition and trans
C;Genetics:
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Nucleic Acids Res. 15, 3961-3976, 1987
A;Title: Nucleotide sequence analysis of the L gene of Newcastle disease virus: homol
A;Reference number: A93665; MUID:87230982
A;Accession: A26747
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A;Reference number: 221598
A;Reference number: 221598
A;Reference number: 221598
A;Reference number: 221598
A;Reference number: 22159
A;Reference nu
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A;Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome polyprotein - Newcastle disease virus (strain Beaudette C)
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: Newcastle disease virus
C:Species: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
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C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
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A;Residues: 1-2204 <YUS>
4;Cross-references: CB:XU53199; NID:g60937; PIDN:CAA28985.1; PID:g60939
(;Genetics:
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                                                                                                                                                                                                                       A.Gene: gpri
F:56-74/Domain: transmembrane #status predicted <TMI>
F:91-109/Domain: transmembrane #status predicted <TM2>
F:139-157/Domain: transmembrane #status predicted <TM3>
F:180-198/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                  F;255-273/Domain: transmembrane #status predicted <TM5>F;622-640/Domain: transmembrane #status predicted <TM6>F;661-679/Domain: transmembrane #status predicted <TM7>
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Pred. No. 2.6e+02;
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Pred. No.
                                                      weid sequence not shown
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Best Local Similarity 66.77
Best Local 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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                                                   A; Status: nucle: A; Molecule type:
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A;Experimental source: strain S288C
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C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 19-May-2000
C;Accession: JC5808
R;Yun, C.W.; Tamaki, H.; Nakayama, R.; Yamamoto, K.; Kumagai, H.
Biocham. Blophys. Res. Commun. 240, 287-292, 1997
A;Reference number: JC5808; MUID:98049822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein YDL035c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein D2749
C.Species: Saccharomyces cerevisiae
C.Species: Saccharomyces cerevisiae
C.Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 29-oct-1999
C.Accession: S67568
R.Paulin, L.; Saren, A.M.; Laamanen, P.
submitted to the Protein Sequence Database, July 1996
A.Reference number: S67560
A.Reference number: S67560
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F:57-73/Domain: transmembrane #status predicted <TM1>
F:92-108/Domain: transmembrane #status predicted <TM2>
F:140-156/Domain: transmembrane #status predicted <TM3>
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Pred. No. 1.9e+02;
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66.7%;
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Best Local Similarity 66.7
Matches 4: Conservative
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Best Local Similarity 66.7
Matches 4; Conservative
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A; Residues: 1-961 <PAU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 4L
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us-09-446-109a-7.rpr

Query Match

82.9%; Score 29; DB 2; Length 119;
Best Local Similarity 66.7%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 1; Indels 9 9

0;

0; Gaps

1 FKPXWR 6 |:| || 36 FEPGWR 41

Search completed: February 27, 2002, 11:45:19 Job time: 698.sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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February 27, 2002, 11:42:44 ; Search time 78.39 Seconds
(without alignments)
2.806 Million cell updates/sec OM protein - protein search, using sw model Run on:

Title: Sorie: 35 Sequence: 1 PRPXWR 6

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 seqs, 36664827 residues Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	P37629 escherichia			-			P97364 mus musculu			P46309 arabidopsis	Q63880 mus musculu			Q03598 caenorhabdi							P79240 pan troglod	wns w			bacillu	gallu	P29043 homo sapien	mus п	P29457 rattus norv	P50454 homo sapien	1854	Q16581 homo sapien	Q05911 saccharomyc
ID	YHIL_ECOLI	PTR2_CANAL	YM91_SCHPO	YHFM_ECOLI	RRPL_NDVB	YEDK_ECOLI	SPS2_MOUSE	YZ64_SYNY3	GSH1_BRAJU	GSH1_ARATH	ESTM_MOUSE	HSPD_BRAJA	HSPH_BRAJA	YLF6_CAEEL	CGC6_HUMAN	DSBA_LEGPN	VENV_BEV	CYPE_DROME	YHJD_ECOLI	C5AR_GORGO	CSAR_PANTR	C5AR_MOUSE	CSAR_HUMAN	C5AR_RAT	DXR_BACSU	HS47_CHICK	HS47_HUMAN	HS47_MOUSE	HS47_RAT	CBP2_HUMAN	RDXA_RHOSH	C3AR_HUMAN	PUR8_YEAST
80	-	-	-			-4	-	-	-		-		-	-	-	-	-	-	-	-	-	_	-	-	-	-	-	-	-	-	-		-
Length	535	623	807	445	2204	217	452	477	514	522	554	151	151	162	167	204													4	41	4	482	482
% Ouery Match	94.3	94.3	88.6	85.7	85.7	82.9	82.9	82.9	82.9	82.9	82.9	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0	80.0		80.0
Score	33	33	31	30	30	53	58	29	58	58	59	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
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023051 arabidopsis	010479 schizosacch	Q9cb81 mycobacteri	P17519 potato leaf	P03357 akr murine	O83728 treponema p	P55465 rhizobium s		Q9xyd3 caenorhabd1			Q50864 myxococcus
C883_ARATH	YDF7_SCHPO	GLPK_MYCLE	V70K_PLRV1	POL_MLVAK	PODK_TREPA	Y4G1_RHISN	Y5G0_CLOAB	HBL1_CAEEL	ATX9 TETTH	POL_MLVAV	RFBC_MYXXA
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88	78	28	28	28	28.	28	28	28	28	28	28

ALIGNMENTS

94.3%;

Query Match

Length 535; DB 1; Score 33;

Matches

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807 AA
                    PRT;
                  STANDARD;
RESULT 3
YM91_SCHPO
ID YM91_SCHPO
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Matches

g ò

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01-NOV-1988 (Rel. 09, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20.5-NG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 91 KDA PROTEIN IN COB INTRON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X02819; CAA26587.1; -.
EMBL; X54421; CAA38288.1; -.
INDEPPO; IPR003615; HNH_Nuc.
INTERFO; IPR000442; INTEOM_MALUSSE2.
INTERFO; IPR000477; RVTSG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01348; Intron_maturas2; 1.
                                                                                                                                                                                                             MEDLINE-86011547; PubMed-4046021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00078; rvt; 1.
                                                                                                                                      Schizosaccharomyces
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 |:
707 FKPSWK 712
                                                                                             Mitochondrion.
                                                                                                                                                                                                                                                                                                                                 STRAIN-AD7-50;
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YHFM_ECOLI
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                                                                                                                                                                                                                                                  Candida albicans (Yeast).
Eukaryota; Hungi; Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                    STRAIN-CBS 562 / ATCC 18804;
MEDLINE-95291458; PubMed=7773409;
MEDLINE-95291458; PubMed=7773409;
Maider P.A., Lubkowitz M.A., Perry J.R., Miller D., Krainer E.,
Naider F.R., Becker J.M.;
"Cloning of a Candida albicans peptide transport gene.";
"Interpolation of a Linia7-1156(1995).
"Interpolation uprake OF SMALL PEPTIDE.
"SUBCELLULAR LOCATION: UPTGRRAL MEMBRANE PROTEIN.
"SUBCELLULAR LOCATION: UPTGRRAL MEMBRANE PROTEIN.
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                  Indels
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1601FD3AE21B80EB CRC64;
                  -;
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                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDE TRANSPORTER PTR2.
                                                                                                                                                 623 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane.
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25;
   ed. No. 22;
Mismatches
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Pred. No. 2
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POTENTIAL.
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POTENTIAL.
    Pred. No.
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PROSITE; PS01023; PTR2_2; 1.
Peptide transport; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69941 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U09781; AAA80167.1; -. InterPro; IPR000109; PTR2.
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.3%;
83.3%;
                5; Conservative
                                                                                                                                                 STANDARD;
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549
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557
623 AA;
 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                             168 FKPDWR 173
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445 FKPIWR 450
                                            1 FKPXWR 6
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                                                                                                                                            PTR2_CANAL
P46030;
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                                                                                                                                                                                                                                                             Lang B.F., Ahne F., Bonen L.;
"The mitochondrial genome of the fission yeast Schizosaccharomyces pombe. The cytochrome b gene has an intron closely related to the first two introns in the Saccharomyces cerevisiae coxl gene.";
J. Mol. Biol. 184:353-366(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
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P45539; P76686;
01-NOV-1995 (Rel. 32, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AuG-2090 (Rel. 40, Last annotation update)
HYPOTHETICAL 47.5 KDA PROTEIN IN CYSG-TRPS INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 807;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00507; HNHc; 1.
Hypothetical protein; Mitochondrion.
SEQUENCE 807 AA; 91637 MW; AFD70F35E84CAA8F CRC64;
                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31; DB 1
Pred. No. 78;
1; Mismatches
Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
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NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 FKPXWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YEDK_ECOLI
P76318;
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P11205;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
STRAIN=K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                  "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. WEDLINE-87230982; PubMed-3035486; WEDLINE-87230982; PubMed-3035486; Vusoff K., Millar N.S., Chambers P., Emmerson P.T.; "Nucleotide sequence analysis of the L gene of Newcastle disease virus: homologies with Sendai and vesicular stomatitis viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein; Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                 (POTENTIAL). SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 1; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Newcastle disease virus (strain Beaudette C/45) (NDV).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 71;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro: IPR002293; AA_rel_permease_1.
Interpro: IPR002027; Amino_acid_permease.
Pfam; PF00324; aa_permeases; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47576 MW;
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66.7%;
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445 AA;
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Best Local Similarity
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381 YKPLWR 386
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                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. There are no restrictions on its use by non-profit institutions and a its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                         FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A) SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAS, RNA BDITING OF THE P GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.
SIMILABRITY: WITH L PK. PECHEN OF OTHER PARAMYXOVIRUSES.
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"Organization of the Escherichia coli and Salmonella typhimurium
chromosomes between flagellar regions IIIa and IIIb, including a
Nucleic Acids Res. 15:3961-3976(1987).
-!- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; ''''.teobacteria; gamma subdivision; Enterobacteriaceae;
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 24.5 KDA PROTEIN IN AMYA-FLIE INTERCENIC REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The profession of the paramyx_RNA_pol.
Interpro: IPO0946; Paramyx_RNA_pol; 1.
Transferase; RNA-directed RNA polymerase.
sponinger 2204 AA; 248822 MW; C6788674D904802C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 1;
Pred. No. 3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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J. Gen. Microbiol. 139:1401-1407(1993).
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STRAIN=K12 / MG1655;
MEDLINE=97426617; Pubmed=9278503;
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Best Local Similarity 66.7
Matches 4; Conservative
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-!- FUNCTION: SYNTHESIZES SELENOPHOSPHATE FROM SELENIDE AND ATP.
-!- CATALYTIC ACTIVITY: ATP + SELENIDE + H(2)O = AMP + SELENOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SELENIDE,WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2)
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENCODED BY THE OPAL CODON, UGA.
SIMILARITY: BELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guimaraes M.J., Bazan J.F., Zlotnik A., Wiles M.V., Grimaldi J.C., Lee F., McClanahan T.:
A new approach to the Study of haematopoietic development in the yolk sac and embryoid bodies.";
Development 121:3335-3346(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97140286; PubMed=8986768;
Guimaraes M.J., Peterson D., Vicari A., Cocks B.G., Copeland N.G.,
Gilbert D.J., Jenkins N.A., Ferrick D.A., Kastelein R., Bazan J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                          Hypothetical protein; Complete proteome.

CONFLICT 213 217 TRARS -> NGCAELIOPV (IN REF. 1).

SEQUENCE 217 AA; 24500 MW; 4F26C95DB3B02900 CRC64;
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                                                                                                                                                                                                                                                                            82.9%; Score 29; DB 1; Length 217; 66.7%; Pred. No. 57; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 AA.
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                    EMBL; L13279; -; NOT_ANNOTATED_CDS.
EMBL; AE000285; AAC74998.1; -.
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InterPro; IPR000728; AIRS_related.
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                                                                                                   DUF159.
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                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                      EcoGene; EG13278; yedk.
InterPro; IPR003738; DU
Pfam; PF02586; DUF159;
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Best Local Similarity
Matches 4; Conserv
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87 FKPLWQ 92
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P97364;
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SPS2_MOUSE
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SO TW DR BY TY SO
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hiyajima N., Hirosawa M., Sayamoto S., Kimura T.,
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
Yasuda M., Tabata S.,
Yasuda M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).
                                          IMPORTANT FOR CATALYTIC ACTIVITY (BY
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                                                                                                                                                                                                           Length 452;
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                                                                                                                                                                                                       Score 29; DB 1; Length 452
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
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Pfam. PF02696; UPF0061; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 477 AA; 54041 MW: 81F6899B1A6D613C CRC64;
                                                                                                                                              9DA6F7250CFE80E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           stis sp. (strain PCC 6803).
Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 29; DB 1; Len
Pred, No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 40, Last annotation update)
HYPOTHETICAL 54.0 KDA PROTEIN SLL1464.
                                                                                ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                               477 AA.
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                                                               SIMILARITY
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    POTENTIAL.
                                                                                                                          POLY-ALA
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                                                                                                                                           47786 MW;
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66.7%;
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66.7%;
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                                                                              328
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440
    63
66
                                                                                                                                              452 AA;
                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSH1_BRAJU
023736; Q43389;
                                                                                                                                                                                                                                                                                                                             48 FSPSWR 53
                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                     1 FKPXWR
                                                                                                                                                                                                                                                                                                                                                                                                                                 Y264_SYNY3
P73436;
ACT_SITE
SE_CYS
SITE
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                                                                                                                                              SEQUENCE
                                                                              NP_BIND
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ID GSH1_B
AC 023736
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core eudicots; Rosidae;

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KK STRAIL-CV. COLUMBIA.

RADIINE-20083488 Pubbwed-10617188.

RADIINE-2008348 RADIINE RADII
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SLUTAMATE--CYSTEINE LIGASE, CHLOROPLAST PRECURSOR (EC 6.3.2.2) (GAMMA-
                            GLUTANYLCYSTEINE SYNTHETASE) (GAWMA-ECS) (GCS).
GSH1 OR AT4G23100 OR F7H19.290.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta: Embryophyta; Tracheophyta:
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Arabidopsis thaliana gamma-glutamylcysteine synthetase is
structurally unrelated to mammalian, yeast, and Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-EV. LANDSBERG ERECTA;
Ullmann P., Gondet L., Bach T.J.;
"Isolation of an Aribidopsis thaliana cDNA encoding a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-glutamylcysteine synthetase by complementation of a GSHI deficient yeast mutant-glutamylcysteine synthetase."; submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The glutathione-deficient, cadmium-sensitive mutant, cad2-1, Arabidopsis thaliana is deficient in gamma-glutamylcysteine syntherace".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 91:10059-10063(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cobbett C.S., May M.J., Howden R., Rolls B.;
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95023984; PubMed-7937837;
May M.J., Leaver C.J.;
                                                                                                                                                                                                                                                                                                                                                COLUMBIA; TISSUE-Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. COLUMBIA;
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                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homologs.
       RANGER RESERVED BY SERVED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See.http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                   15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUTAMATE--CYSTEINE LIGASE, CHLOROPLAST PRECURSOR (EC 6.3.2.2) (GAMMA-GLUTAMAYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schaefer H.J., Haag-Kerwer A., Rausch T.; "coNk cloning and expression analysis of genes encoding GSH synthesis in roots of the heavy-metal accumulator Brassica juncea L.: evidence for Cd-induction of a putative mitochondrial gamma-glutamylcysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
MISCELLANEOUS: IN PLANTS, THERE ARE TWO FORMS OF THIS ENZYME, ONE
CYTOSOLIC AND THE OTHER CHLOROPLASTIC.
                                                                                                                                                                                                                                        Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schaefer H.J., Greiner S., Rausch T., Haag-Kerwer A.;
"In seedlings of the heavy metal accumulator Brassica juncea, Cu2+
differentially affects transcript amounts for gamma-glutamylcysteine
synthetase (gamma-ECS) and metallothiconein (MT2).";
FEBS Lett. 404.216-220(1997).
-!- CATALYTITY: ATP + L-GLUTAMATE + L-CYSTEINE - ADP +
ORTHOPHOSPHATE + GAMMA-L-GLUTAMATL-L-CYSTEINE.
-!- PATHWAY: FIRST AND RATE-LIMITING STEP IN DE NOVO GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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TRANSIT 1 55 CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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-> I (IN REF. 2).
-> T (IN REF. 2).
07C71CB13E785FA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ***********
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. VITTASSO; TISSUE-Leaf; MEDLINE-97227950; Pubmed-9119067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-98281577; PubMed-9620267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Mol. Biol. 37:87-97(1998).
       Created)
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       15-DEC-1998 (Rel. 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthetase isoform.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 ;
514 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-3707;
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204 FQPKWR 209
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2

RESULT

a ò

Matches

GSH1_ARATH

32555

CHAIN

of

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MEDLINE-93:25638; PubMed-7916639;
                                                                                                                                                                                                                                                                                                                                           RETICULUM
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069241;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
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A EMBL; 229490; CAA82620.

JR EMBL; ALO81018; CAA19826.1: -.

DR EMBL; ALO131018; CAA19826.1: -.

DR EMBL; ALO131018; CAA19826.1: -.

DR EMBL; ALO131018; CAA19826.1: -.

DR Mendel; 33329; Arath; 2621:3329.

DR Mendel; 33329; Arath; 2621:3329.

DR Mendel; 36322; Arath; 2621:3329.

Mendel; 36322; Arath; 2621:36232.

KW Glutathione biosynthesis: Ligase; Chloroplast; Transit peptide.

FT TRANSIT 1 CHLOROPLAST (POTENTIAL).

TRANSIT 2 2 CHUCNOPLAST (POTENTIAL).

TRANSIT 1 CHLOROPLAST (POTENTIAL).

TAAIN 2 22 A -> T (IN STRAIN LANDSBERG ERECTA).

48 Y -> N (IN STRAIN LANDSBERG ERECTA).

TACGEALGOVQRANGTKRRSRVRRAAVLRWDVNKRCL

TANDSBERG ERECTA).

TANDSBERG ERECTA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ES-MALE) (ESTERASE-31).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SUBGUNIT: MONOMER (PROBABLE).
-:- SUBCELLULAR LOCATION: CHLOROPLAST (PROBABLE).
-:- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND ROOTS.
-:- HISCELLANEOUS: IN PLANTS, THERE ARE TWO FORMS OF THIS ENZYME, ONE CYTOSOLIC AND THE OTHER CHLOROPLASTIC.
Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Antonotu B., Zidanic M., Jones K., Drone K., Cotton M., Joshu C., Antonotu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M., Martienssen R., McCombie W.R.; Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                            NALLIE 402:769-777(1999).

-!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + L-CYSTEINE = ADP +
ORTHOPHOSPHATE + GAMMA-L-GLUTAMYLL-CYSTEINE.

-!- ENZYME REGULATION: FEEDBACK INHIBITION BY GLUTATHIONE.
-!- PATHWAY: FIRST AND RATE-LIMITING STEP IN DE NOVO GLUTATHIONE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BALB/CJ X DBA/2J; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BIOSYNTHESIS
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212 FOPKWR 217
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TD ESTM_MOUSE
AC 063880;
DT 01-NOV-1997

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as part of
                                                                                                                                                                                       + A CARBOXYLIC ANION.
-i- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE, LUMEN OF ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
LIVER CARBOXYLESTERASE.
BY SIMILARITY.
PREVENT SECRETION FROM ER (POTENTIAL).
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
Endoplasmic reticulum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Narberhaus F., Weiglhofer W., Fischer H.M., Hennecke H.;

Narbertlication of the Bradyrhizobium japonicum degp gene as pair

"Identification of the Bradyrhizobium japonicum degp gene as pair

an operon containing small heat shock protein genes.";

Submitted (NOV-1997) to the EMBL/GenBank/DDBJ detabases.

-: SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     028D898B06F3CAAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 29; DB 1;
Pred. No. 1.3e+02;
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30-MAY-2000 (Rel. 39, Last annotation update)
SMALL HEAT SHOCK PROTEIN HSPD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WGD; MGT.102773; ES31.
InterPro; IPR002018; Carboxylesterase_B.
InterPro; IPR000379; Est_lip_thloest_actsite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1. PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Hydrolase; Serine esterase;
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30-MAY-2000 (Rel. 39, Last sequ
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00135; COesterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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215
443
110
278
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=375;
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80.0%;
80.0%;
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                                    STANDARD;
                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 STRAIN-BRISTOL N2
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                                                                                                                                                                                               NCBI_TaxID=6239;
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                                   YLF6_CAEEL
Q03598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans.
                                                                                                                               C40H1.6
     RESULT 14
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                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muenchbach M., Nocker A., Narberhaus F.;
"Occurrence of a superfamily of small heat shock proteins in
Bradyrhizobium japonicum and other Rhizobium species: a plant-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Bradyrhizobium group; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                              80.0%; Score 28; DB 1; Length 151; 66.7%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                               FB44EF94FB599EE4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 64;
0; Mismatches
                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ010144; CAA09014.1; -.
InterPro; IPR002068; Crystallin_HSP20.
Pfam; PF00011; HSP20; 1.
                                                                                                                                            InterPro) IPR002068; Crystallin_HSP20.
Pfam: PF00011; HSP20; 1.
PROSITE; PS01031; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                               Heat shock; Multigene family.
SEQUENCE 151 AA; 17272 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMALL HEAT SHOCK PROTEIN HSPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 AA; 17098 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat shock; Multigene family.
                                                                                                                                 EMBL; AJ003064; CAA05835.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01031; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bradyrhizobium japonicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.0
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conserv
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6 FSPLWR 11
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6 FSPLWR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                           HSPH_BRAJA
086110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
HSPH_BRAJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Johnston L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latrellie P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;;
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                                                                      01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 18.5 KDA PROTEIN C40H1.6 IN CHROMOSOME·III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WormPep; C40H1.6; CE00114.
Hypothetical protein.
SEQUENCE 162 AA; 18537 MW; 8DC03CE3BCE79D55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994).
-!- SIMILARITY: STRONG, TO HUMAN CGI-126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCCC_HUMAN STANDARD; PRT; 167 AA. 09Y3C8; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) APPOTHETICAL PROTEIN CGI-126.
   162 AA.
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PRT;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
MEDLINE-20272150; PubMed-10810093; Lai C.-S., Lin W.-C.: Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.: Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics."; Genome Res. 10:703-713(2000).
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                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 167 AA; 19458 MW; 1675D9187DC43E14 CRC64;
                                                                                                                                                                                                                                                                                                                              EMBL; AF151884; AAD34121.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
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Search completed: February 27, 2002, 11:42:45 Job time: 544 sec

1 FKPXW 5

ò g emericella streptomyce klebsiella

29xaa5

Sequence:

Run on:

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Searched:

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"DNA seque and genetic organization of the integron-carrying Replasmid of the Corynebacterium glutamicum."; Submittee "11.1999) to the EMBL/GenBank/DDBJ databases. EMBL: AFI . 55; AGG00294.1; Interpro: 10.002145; CopG_HTH_4. Plasmid.
                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes, Actinobacteria, Actinobacteridae,
Actinomycetales, Corynebacterineae, Corynebacteriaceae,
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                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                Corynebacterium glutamicum (Brevibacterium flavum).
Plasmid R-plasmid pCG4.
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83.3%; Pred. No. 35;
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09FND2
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022568
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09YG81
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Q9F2R9
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Matches 5; Conserv
                        Corynebacterium.
NCBL_Taxff :7'8;
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214 FKPAWR 219
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SEQUENCE
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090341 newcastle d
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0901d3 newcastle d
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09vy94 drosophila
                                                                   (without alignments)
3.115 Million cell updates/sec
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                                                           February 27, 2002, 11:50:07; Search time 281.76 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                        473505 seqs, 146272329 residues
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Listing first 45 summaries

    protein search, using sw model

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Q9XYP8
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Gapop 10.0 , Gapext 0.5
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Q12361
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sp_vertebrate:*
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sp_phage:*
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: sp_bacteria:*
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Maximum DB seq length: 200000000
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85.
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Result

250 AA.

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380 AA

Length 250; Indels

09c1b2 gibberella 09d088 fusarium sp 09c1b9 fusarium sp 09kn89 vibrio chol 04014 nicotiana s 052729 rhizobium e 09yg81 aeropyrum p 09hc7 pseudomonas 042902 schizosacch

0926w4 klebsiella 096402 plasmodium 096102 plasmodium 090191 glardia lam 090296 caenorhabdi 091296 caenorhabdi 091298 treptomyce 091878 triticum ae 091002 leishmania 02358 caenorhabdi 026470 methanobacter 09710 caulobacter 09710 caulobacter 09710 aethanobacter 09710 aethanobacter 09710 aethanobacter 09710 aethanobacter 09710 aethanobacter 09710 aethanobacter

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SEQUENCE 498 AA
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445 FKPIWR 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- COFACTOR: NICKEL (BY SIMILARITY).
-1- PATHWAY: HYDROGEN METABOLISM; FHL PATHWAY (BY SIMILARITY).
-1- SUBUNT: FHL COMPRISES OF A FORMATE DEHYDROGENASE, UNIDENTIFIED ELECTRON CARRIERS AND A HYDROGENASE (ISOENZYME 3). IN THIS NON-FONEMY CONSERVING PATHWAY MOLECULAR HYDROGEN AND CARBODIOXIDE FROM FORMATE ARE RELEASED (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE COMPLEX I 49 KDA SUBUNIT FAMILY.
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE FORMATE HYDROGENLYASE SUBUNIT 5 (FHL SUBUNIT 5) (HYDROGENASE-
                                                                                                                                                                                                                                            SECUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-9637999; Pubmed-8688087;
MEDLINE-9637999; Pubmed-8688087;
MELON G.G., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Webinstock K.G., Werrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nduyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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MEDLINE-98332770; PubMed-9665876;
MEDLINE-98332770; PubMed-9665876;
M. NORTHIS S.J., Weinstook G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Retchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR001135; Complex1_49kd.
InterPro: IPR001501; NIFESE_Hases.
InterPro: IPR001501; NIFESE_Hases.
Pfam: PF00314; Complex1_49kd; 1.
PR0SITE: PS00505; NI_HESE_HASEs: 1.
PROSITE: PS00507; NI_HERNSE_L_1; UNKNOWN_1.
PROSITE: PS00507; NI_HERNSE_L_1; UNKNOWN_1.
PROSITE: PS00507; NI_HERNSE_L_1; UNKNOWN_1.
NICKE1: Complete proteone.
SEQUENCE 380 AA: 43638 MW: 3EAD16D67834A76F FRF64.
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                                                                                                                                         Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U67501; AAB98504.1;
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01-NOV-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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Matches 5; Conserv
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241 FKPVWR 246
                                                                                              3 COMPONENT E).
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Knalak H. .currib., Howell J.K., Chidamb. M., Utterback T., McDonald .relack P., Bowman C., Cotton M.D., Pujii C., Garland S., Hatch B., Hotst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tait E., Simon M.C., King S., Brown A.J., Gow N.A.K., Shaw D.J.; "A Candida albicans Genome Project: Cosmid Contigs, Physical Mapping, and Gene Isolation.";
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                       "Complete genome sequence of Treponema pallidum, the syphilis
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrell B.G., Rajandream M.A.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fungal Genet. Biol. 21:308-314(1997).

EMBL, AL033503; CAA2021.1; -.

InterPro; IPR00109; PTR2.

PROSTITE; PS01022; PTR2.1; 1.

PROSTITE; PS01023; PTR2.2; UNKNOWN.1.

SEQUENCE 623 AA; 69943 MW; 8543A3B1F7E7363E CRC64;
                                                                                                                                                                                                                                                                                498 AA; 56074 MW; 81710E41264431B8 CRC64;
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Last annotation update)
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Pred. No. 1.3e+02;
O; Mismatches L;
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Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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83.3%;
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                                                                                                                                                                  EMBL; AE001251; AAC65773.1;
TIGR; TP0806; -.
                                                                                                                                                                                                              InterPro; IPR003447; FemAB.
Pfam; PF02388; FemAB; 1.
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Best Local Similarity 83...
Best Local 5; Conservative
                                                                                                                                                Science 281:375-388(1998)
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Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
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Best Local Similarity
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657 FKPLWR 662
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Man K.H., Doyle C., Bazer E.G., Helt G., Nelson C.R., Mikklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Bocchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Borkova D., Bocchan M.R., Bulke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Borkova D., Borlet A., Dong Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M., Glasser K.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L(1)DD4 OR CG10988.
Drosophila melanogaster (Fruit fly).
Bukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae: Drosophila.
                                                                                                                                         Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha: Ephydroidea: Drosophilidae: Drosophila.
NCBL_TaxiD=7227;
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                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-99156983; PubMed-10037793;
OGGEME K., Jwamatsu A.,
Mitchison T.J., Zheng Y.;
"Characterization of two related Drosophila gamma-tubulin complexes that differ in their ability to nucleate microtubules.";
EMBL, AF118380; AAD27817.11;
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                                                       01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GAMMATUBULIN RING PROTEIN DGRIP91.
L(1)DD4 OR DGRIP91 OR CG10988.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                            94.3%; Score 33; DB 5; Length 917;
83.3%; Pred. No. 1.9e+02;
ive 0; Mismatches 1; Indels
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Interpro: IPR000634; dehydrtse_ser_thr.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
SEQUENCE 917 AA: 103819 MW: EBF2F41E35049D27 CRC64;
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                PRT;
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                                           (TrEMBLrel. 12,
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Best Local Similarity 83.3
Matches 5; Conservative
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                PRELIMINARY;
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657 FKPLWR 662
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01-NOV-1999 (
01-JUN-2001 (
                             09XYPB;
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Q9VY94;
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A Jalain M., Kalush F., Krapen G.H., Ke2., Kennison J.A., Ketchum K.A., A Jalain M., Kalush F., Krapen G.H., Ke2., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., A Liu X., Matteel B. McIntosh T.C. McLedd M.P., McPherson D., A Musteel B. McIntosh T.C. McLedd M.P., McPherson D., A Musteel B., McIntosh T.C. McLedd M.P., McPherson D., A Musteel B., McIntosh T.C. McRed M.P., McPherson D.C., McMan M. Musphy B., Muskern D.R., Nelson D.E., Nixon K., Nixon K., Nixon K., Nixon K., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., A Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T., A Spier E., Spradling A.C., Stapleton M., Stroug R., Sun E., Spier E., Spradling A.C., Stapleton M., Stroug R., Sun E., Mang Z.-Y., Wassarman D.A., Weischock G.M., Weissenbach J., Mulliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., A Loheng X.H., Zhong F.W., Zhong F.W., Zhong W., Zhang C., Zhao G., Zheng C., The Genome Sequence of Drosophila melanogaster.";

EMBL, ABO03493; AR44839911; ...
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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Sasaki T., Nagamura Y., Yamamoto K.;
Sasaki T., Nagamura Y., Yamamoto K.;
"Oryas activa nipponbare(GA3) genomic DNA, chromosome 6, PAC clone:P0680A03.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB023482; BAA78741.1; - CEMBL, AB023482; BAA78741.1; - SEQUENCE 221 AA, 24502 WW; DC24FF370660BC15 CRC64;
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PROSITE; PS00165; DEHYDRATASE_SER_THR: 1.
SEQUENCE 917 AA; 103706 MW; 6AEE88C211D256BB CRC64;
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EMBL; AP000060;
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K MEDLINE-21065660; PubMed=11217851;

K MANA J., Shinagama A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

K Awal J., Shinagama A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

R Alto T., Okazaki Y., Golobori T., Bono H., Kasukawa T., Salto R.,

R Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

R Adota K., Matsuda H.A., Ashburner M., Batalov S., Casavant H.,

R Achini L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

R Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

R Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

R Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

R Doors P., Marchloni L., Mashima J., Mazzarelli J., Mombaerts P.,

R Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

R Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

R Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

R Storch M., Parchiola C., Parking M., Charles C., Whittaker C., Whilming L.,

R Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Whilming L.,

R Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Whitming L.,

R Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Whitming L.,

R Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Whitming L.,

R Suzuki H., Toyo-oka K., Wang K.H., Waltz C., Whittaker C., Whitming L.,

R Suzuki H., Sato K., Schoenbach C., Waltz C., Whiteles C., Whiteles C., Whiteles C., Whiteles C., Whitming L.,

R Suzuki H., Sato K., Schoenbach C., Waltz C., Whiteles C., Wh
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                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Functional annotation of a full-length mouse cDNA collection.";
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
5830420220RF PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 24.8 KDA PROTEIN APE0766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99310339; PubMed-10382966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mature 409:685-690(2001).
EMBL; AK017942; BAB31014.1; -.
MGD; MGI:1923275; 5830420C20Rik.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1923275;
SEGUENCE 204 AA
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NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                       5830420C20RIK.
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29 FRPRWR 34
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109 YESULT
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Arakava T., Hara A., Shibata K., Yoshino M., Ishii Y.,
Arakava T., Hara A., Shibata K., Yoshino M., Ishii Y.,
Arakava T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Alzawa K., Izawa M., Nishi K., Kiyosawa H., Rondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Rasukawa T., Saito R.,
A Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuchi P., Lewis S., Macsuo Y., Nikaido I., Pesole G., Quackehoush J.,
Schrim L.M., Staubli F., Sizuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibodi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Functional annotation of a full; length mouse cDNA collection.";
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66.7%; Pred. No. 3.5e+02;
Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TremBirel 17, Last sequence update)
01-JUN-2001 (TremBirel 17, Last annotation update)
ADULT MALE TESTIS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE: 17,000300120, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                  Length 239;
                                                                                                                                                                                                                                                                                                                Indels
                                                    Pfam: PF00702; Hydrolase; 1.—PR057TE; PS01229; COF-2; UNKNOWN_1.
Hypothetical protein: Complete proteome.
SEQUENCE 239 AA; 24758 MW; EA30A3CDFD86B3DE CRC64;
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Pred. No. 1.9e+02;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
InterPro; IPR001454; Hydrolase.
InterPro; IPR000150; Hypothet_cof.
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EMBL; AKO06565; BAB24655.1; -.
MCD; MCI:1923275; 5830420C20Rik.
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                         105 FKPSWQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y.;
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(without alignments)
3.115 Million cell updates/sec
                                                                   February 27, 2002, 11:50:07; Search time 281.76 Seconds
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                - protein search, using sw model
                                                                                                                                                                                                                                                                     SPTREMBL_17:

1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_tungi:*
4: Sp_human:*
5: Sp_nowertebrate:*
6: Sp_mammal:*
7: Sp_anc:
: Sp_organelle:*
: Sp_organelle:*
: Sp_organelle:*
: Sp_organelle:*
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                              sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                       sp_rodent: *
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                                                                                                          Title:
Perfect score:: Sequence:
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                                                  OM protein
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                                                                                                                                                                                                                                                                                            Database
                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Q9eum2 corynebacte	Q57935 methanococc	083784 treponema p	Q9url7 candida alb	Q9xyp8 drosophila	09vy94 drosophila	Q9xj12 oryza sativ	Q9d3f2 mus musculu	Q9ye03 aeropyrum p	Q9d9rl mus musculu	031566 bacillus su	O52961 bacillus su	Q9na80 caenorhabdi	Q12361 saccharomyc	Q91jql arabidopsis	090341 newcastle d	Q9wmh6 newcastle d	v9dld3 newcastle d	Oguvp2 emericella
SUMMARIES			9	09EUM2	057935	083784	Q9URL7	Q9XYP8	Q9VY94	09XJ12	Q9D3F2	O9YE03	Q9D9R1	031566	052961	Q9NA80	012361	106,160	090341	9ншм60	G9DLD3	O9UVP2
			HCI	. ~	-	~	٣	S	S	10	11	-	11	7	~	ហ	m	10	12	12	12	m
			Match Length DB	250	380	498	623	917	917	221	204	239	440	909	610	684	961	1232	2204	2204	2204	2454
	œ	Query	Match	97.1	94.3	94.3	94.3	94.3	94.3	88.6	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7
			Score	34	33	33	33	33	33	31	30	30	30	30	30	30	30	30	30	30	30	30
		Result	Q	1	7	9	4	'n	9	7	æ	5	10	=	12	13	14	15	16	17	18	19

729 729 727 727 729 729 729 729	042902 schizosacch				inae; Seae;	yron-carrying K- bases.	264;	Length 250; ; Indels 0; Caps		
9990/55 9950/55 9950/56 9950/71 9960/71 9960/71 9960/71 9960/71 9960/75 9960/75 9960/75 9960/89 9940/89 9940/89 9940/89 9940/89 9940/89 9940/89	042902 ALIGNMEN''S	PRT; 250 AA.	Created) Last sequence update) Last annotation update)	YCG4L. YCG4L. Coryncbacterium glutamicum (Brevibacterium flavum). Plasmid R-plosmid pCG4.	obacteria; Actimobacteriacieri	SEQUENCE FROM N.A. STRAIN=ATCC31830: A Tauch A., Puebler A., Kalinowski J.; Think sequence, and genetic organization of the integron-carrying K-rylax sequence, and genetic organization of the integron-carrying K-rylax sequence, and genetic organization of the integron-carrying K-rylax sequence, and genetic organization (JUL-1999) to the EMBL/GenBank/100BJ databases. R EMBL; AF164956; ARG00294.1: R EnterPro: IPR00145; CopG_HTH_4.	м; 195C86367B483157 СК	Score 34; DB 2; Lenk Pred. No. 35; 0; Mismatches 1;		PRT; 380 AA.
245.4 2 4 4 4 4 2 3 4 4 4 4 2 3 4 4 4 4 4 4	.9 557 3	PRELIMINARY;	(TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 17,	ium glutamicum asmid pCG4.	rmicutes; Actin les; Corynebact ium. 718;	M N.A. 1830; ehler A., Kalin, o and genetic o of Corynebacte Ui1999) to the 55; AAG00294.1; 75; AAG02145; COPG_H 2; HTH_4: 1.	50 AA; 28804 M	97.1%; larity 83.3%; Conservative	5 219	PRELIMINARY;
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	53	SULT 1 SUM2 Q9EUM2	AC Q95UM2; DT 01-MAR-2001 DT 01-MAR-2001 DT 01-JUN-2001		O. Bacteria; Firmicul OC Actinomycetales; C Corynebacterium. OX MCBL_TaxID=1718; RN :11	RP SEQUENCE FROM RR STRAIN-ATCC3 RR TANA ATCC3 RT DLASMIC PCG4 RT DLASMIC PCG4 RL Submitted (U) DR EMBL AF1649 DR PLAYER PC0140 DR PLAYER PC0140	SQ SYQUENCE 2	Query Malch Best Local Similarity Matches 5; Conser	Oy T PKPXWR 111 11 Ob 314 PKPAWR	RESULT 2 057933 UD 357935 AC 057935;

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PRT;
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                                                                       spirochete.";
Science 28:1375-388(1998).
EMBL AE001251; AAC65773.1; -.
TIGR: TP0806; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.3%;
83.3%;
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Similarity 83.3%;
5; Conservative (
                                                                                                                            InterPro; IPR003447; FemAB.
Pfam; PF02388; FemAB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE TRANSPORT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Gene Isolation.";
                                                                                                                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                      Complete proteome. SEQUENCE 498 AA;
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                                                                                                                                                                                                                                                                              111 11
240 FKPKWR 245
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FRPIWR 450
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                                                                                                                                                                                                                                                                                                                                                                         Q9URL7;
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                                                                                                                                                                                                                                   Matches
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09URL7
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O
                                                                                                                                                                                                                                                                                                                         SCIENCE 273:1058-1073(1996).
-!- COFACTOR: NICKEL (BY SIMILARITY).
-!- PATHWAY: INTROGEN METABOLISM: FHL. PATHWAY (BY SIMILARITY).
-!- SUBUNT: FHL COMPRISES OF A FORMATE DEHYDROGENASE, UNIDENTIFIED ELECTRON CARRIERS AND A HYDROGENASE (ISOBNZYME 3). IN THIS NON-ENERGY CONSERVING PATHWAY MOLECULAR HYDROGEN AND CARBODIOXIDE FROM
01-JAN-1998 (TrimmLirel, 05, Created)
01-JAN-1998 (TrimmLirel, 05, Last Sequence update)
01-JUN-2001 (TrimmLirel, 17, Last annotation update)
PUTATIVE FORMATE HYDROGENLYASE SUBUNIT 5 (FIL SUBUNIT 5) (HYDROGENASE-
                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-JAL-1; DSM 2661 / ATCC 43067;
MEDLINE-96337999; PubMed-8688087;
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Flizderald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Frhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Potterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98332770; PubMed-9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Soderyren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00346; complex1_49Kd.1.
Pfam; PF00374; NIFeSe_Hases: 1.
PROSITE: PS00535; COMPLEX1_49K, UNKNOWN_1.
PROSITE: PS00507; NI-HIGBNASE_L.1: UNKNOWN_1.
Hypothetical protein: Oxidoreductase; NAD; Iron-sulfur; 4Fe-4S;
                                                                                                                                                                                                                                                                                                                                                                                                          FORMATE ARE RELEASED (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE COMPLEX I 49 KDA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                 Methanococcus jannaschii.
Archaea: Kuryarchacota: Methanococcales: Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94.3%; Score 33; DB 1; Length 380; 83.3%; Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 AA; 43638 MW; 3EAD16D67834A76F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001135; Complex1_49Kd.
InterPro; IPR001501; NiFeSe_Hascs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nickel; Complete proteome.
SEQUENCE 380 AA; 43638
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U67501; AAB98504.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEMA PROTEIN, PUTATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID-2190;
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241 FKPVWR 246
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                                                      COMPONENT E)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 FKPXWR 6
                                                                                                            Methanococcus
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Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Howman C., Cotton M.D., Fujii C., Carland S., Ilatch B., Horst K., Roberts K., Sandusky M., Weldman J., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tait E., Simon M.C., King S., Brown A.J., Gow N.A.R., Shaw D.J.:
"A Candida albicans Genome Project: Cosmid Contigs, Physical Mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TaxID=5476;
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                                                                                                                      "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                     498 AA; 56074 MW; 81710E41.264431H8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fungal Genet. Biol. 21:308-314(1997).

EMBL; AL033503; CAA22021.1; -

InterPro: IPR000109; PTR2.

PFAR: PFO0854; PTR2.1: 1.

PROSITE; PS01022; PTR2.1: 1.

PROSITE; PS01023; PTR2.2; UNKNOWN_1.

SEQUENCE 623 AA: 69943 MW; 8543A381F7E7363E CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Pred. No. 1.3e+02;
0; Mismatches 1;
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Pred. No. le+02;
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PRT;
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66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Actal Similarity 83.3
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN.
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Bost Lonal Similarity
Matches 4; Conserv
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202 FRPTWR 208
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657 FKPLWR 662
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0903F2;
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09XJ12
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Am K.H., Doyle C., Batzer E.G., Helt G., Nelson C.R., Miktos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Barandale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Bernan B.P., Bhandari D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
A Dorkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
A de Pablos H., Deicher A., Deng Z., Mays A.D., Dow f. Dietz S.M.,
A de Pablos H., Deicher A., Dong Z., Mays A.D., Dow f. Dietz S.M.,
A bodson K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Ry Glodek A., Cong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                           01-NOV-1999 (TrEMBLEEL. 12, Last sequence update)
01-JUN-2001 (TrEMBLEEL. 17, Last annotation update)
CAMMA-TUBULIN RING PROTEIN DGRIP91.
CLAINDA ON DGRIP91 OR CC10988.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazaa; Arthropoda; Tracheata; Hexapoda; Insecta;
Epteryota; Neoptera: Endopleryota; Diplera; Brachycera; Muscomorpha;
Ephydroliges; Drosophilidae; Drosophila.
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Ephydroidea; Drosophilidae; Brosophila.
NCBL_TaxID-7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-99156983; PubMed-10037793;
OGGEMA K., Wiese C., Martin O., Milligan R.A., Iwamalsu A.,
Mitchison T.J., Zheng Y.;
"Characterization of two related Drosophila gamma-tubulin complexes
that differ in their ability to nucleate microtubules.";
EMBL: AF118360; AAD27817.1;
Flybase; FB000001612: 1(1)d44.
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Pred. No. 1.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; iPk000634; dehydrtse_ser_thr.
PROSITE; PS00165: DEHYDRATASE_SER_THR; 1.
SEQUENCE: 917 AA; 103819 MW; EHF2F41E35049D27 CRC64;
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01-MAY-2000 (TrEMHIREL 13, Last sequence update)
01-JUN-2001 (TrEMBLREL 17, Last annotation update)
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                                              917 AA
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Drosophila melanogaster (Fruit fly).
                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.3
Best Local Similarity 83.3
Matches 5; Conservative
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                                                                                                                         01-NOV-1999 (TrEMBLrel. 01-NOV-1999 (TrEMBLrel.
                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Drc
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1D 09XYP8:
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Shrhartoideae: Oryzeae; Oryzea.
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Sasaki T., Nagamura Y., Yamamolo K.;
"Jryka sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
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Pred, No. 1.2e+02;
1; Mismatches 1; Indels
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83.3%; Pred. No. 1.9e+02;
Live 0; Mismatches 1; Indels
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EMBL, AB023482; BAA78741.1; -
SEQUENCE 221 AA; 24502 MW; DC24FF370660BC15 CRC64;
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InterPro: IPR000634; dehydrtse_ser_thr.
PROSITE: PS00165; DEHYDRATASE_SER_THR; l
SEQUENCE 917 AA; 103706 MW; 6AEE88C2110256BB CRC64;
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Arakawa T., Shinadawa K., Shibala K., Yoshino M., Iloh M., Ishii Y.,
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Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
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Sakai K., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,
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A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
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A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Sasaki H., Sato K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Whynshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Whanshaw-Bootis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Mammalia; Eutheria; Rodenlia; Sciurognathi; Muridae; Murinae; Mus
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1: Mismatches 1: Indels
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EMBL; AK017942; BAB31014:1; -.
MGD; MGI:1922275; SB30420C20R!K.
GFOHENCE 204 AA; 22892 MW; 98AF03DF7FC7B066 CRC64;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CS/BL/6J; TISSUE-THYMUS;
MEDLINE-271085660; Pubmed-11217851;
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MEDLINE=99310339; Pubmed=10382966;
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Best Local Similarity 66.7%;
Matches 4; Conservative
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                                                                                      5830420C20RIK PROTEIN.
5830420C20RIK,
                                                                                                                                                             Mus musculus (Mouse)
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                                                                                                                                                                                                                                                   NCB1_Tax1D=10090;
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29 FRPRWR 34
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MEDLINE=21085660; PubMed=11217851;

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MEDLINE=21085660; PubMed=11217851;

MEDLINE=21085660; PubMed=11217851;

MEDLINE=21085660; PubMed=11217851;

MARAWA T., Ilara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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Schriml L.M., Staubil F., Suzuki R., Tomita M., Wagner L., Washio T.,

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Lyons P., Marchionni L., Mamanima J., Mazzarelli J., Mombaerts P.,

Casari H., Sahamoto N.,

Casari H., Sahamot
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Pred. No. 3.5e+02;
1; Mismatches 1; Indels
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01-JUN-2001 (TremBLrel. 17, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
ADULT MALE TESTIS CDNN, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:1700030N20, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 1; Length 239;
Pred. No. 1.9e+02;
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EMBL; AP000060; BAA79744.1; ...
InterPro; IPR001454; Hydrolase.
InterPro; IPR000150; Hypothet_cof.
Pfam, PF00702; Hydrolase; 1.
PROSTITE; PS01229; COF_2; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 239 AA; 24758 MM; EA30A3CDFD86B3DE CRC64;
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EMBL: AK006565; BAB24655.1; -..
MCD: MGI:1921275; 5830420C20Rik.
SEOUENCE 440 AA; 49566 MW; 5B5DA87E19879644 CRC64;
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39 FRPRWR 44
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MEDIANE=97101647; PubMed-8946165; Sanamoto H., Uchiyama S., Sekiguchi J.; Annamoto H., Uchiyama S., Sekiguchi J.; "Cloning and sequencing of a 27.8-kb nucleotide sequence of the 79-legrees-81 degrees region of the Bacillus subtilis genome containing DNA Res. 3:257-262(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota: Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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Saccharomycofales, Saccharomycotaceae, Saccharomyces,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%; Score 30; DB 5; Length 684; 66.7%; Pred. No. 5.3e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans: A platform tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 2; Length 610;
Pred. No. 4.7e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ...vestigating biology.";
Seiber 282:2012-2018(1998).
Seiber 41,11715, CABS5023.1; -
SEQUENCE 684 AA; 79659 MW; FOEAFAF2BEAFF687 CRC64;
                                                                                                                                                                                                                                                                                                                                                           EMBL; D85082; BAA24464.1; -. 34094DD5CA72FF66 CRC64; SEQUENCE 610 AA; 69089 MW; 34094DD5CA72FF66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TREMBLREL. 17, Last annotation update)
01-JUN-2001 (TREMBLREL. 17, Last annotation update)
03-JUN-2001 (TREMBLREL. 10, TREMBLREL. 10, TREMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.- e.T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
91-MAR-2001 (TrEMBLrel. 16, Last annotation update)
      Macteria, Firmicutes, Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        684 AA.
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                           Proillus/Staphylococcus group; Bacillus.
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66.7%;
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Best Local Similarity burea
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:72 FKPKWK 677
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Q12361;
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Q12361
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Submitted (MOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 299108; CAB12672.1; -.
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Last annotation update)
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NCBI_TaxID+1423;
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U31566;
01-JAN-1998 (TrEMBLREL: 05,
01-JAN-1998 (TrEMBLREL: 05,
01-NOV-1998 (TrEMBLREL: 08,
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Matches 4; Conservalive
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01-JUN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                Bacillus subtilis.
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570 YKPEWR 575
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                                                                                                                                   YFIX PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-168;
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Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
TAC and BAC clones.";
DNA Res. 7.217-221(2000).
-1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
EMBL. AP000414: DAD01179-1;
-1 nterPro: IPR000194: AFPBS-2 alpha_beta.
InterPro: IPR000195: CytC_heme_bind.
InterPro: IPR000185: CytC_heme_bind.
Pfam: PF00097: z1-C3HC4: 1.
SMART: SM00184: RING: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thallana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae:
eurosids II; Brassicates: Brassicaceae: Arabidopsis.
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-COLUMBIA;
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted.(SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       .
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                                                                                                                                                                                                                                                                                                      Score 30: DB 3: Length 961:
Pred. No. 7.3e+02:
1: Mismatches 1: Indels
                         SEQUENCE FROM N.A.
STRAIN-ALPHA S288C;
Paulin L., Saren A.M.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D3770C4A9D699207 CRC64;
                                                                                                                                                                        MIPS; ... 171781. CAA96454.1; -.. EMBL/GenBank/DDBJ databases. Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. 271781. CAA98543.1; -. SGD: SO002193. GPR1. Hypothetical protein. SEQUENCE 961 AA; 110708 MW; 9889D857872A4209 CRC64;
                                                                                                                Paulin L., Saren A.M., Laamanen P.;
Submitted (JUL-1996) to the EMBL/GenBank/DDDJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-001.
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last scaucnce update)
01-0CT-2001 (TrEMBLrel. 17, Last annotation update)
GHJANN55299.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS00152; ATPASE_ALPHA_BETA: UNKNOWN_1.
PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 1232 AA.
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                                                                                                                                                                                                                                                                                                       85.7%;
                                                                                                                                                                                                                                                                                                                     Best Local Similarity 66.7
Matches 4; Conservative
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PubMed-10907853;
NCBI_Tax1D+4932;
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Score 30; DB 10; Length 1232; Pred. No. 9.2c102; 1; Mismatches 1; Indels

Query Malch Host Local Similarity 66.7%; Matches 4; Conservative

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Qy 1 PKPXWR 6
111 1:
Db 902 PKPGWK 907
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Search completed: February 27, 2002, 11:50:09 Job time: 988 sec

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FILING DATE: CLASSIFICATION: 435
ATTORNEY/A FAT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                     US-08-215-137-13
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Sequence 2, Appli
Sequence 3, Appli
Sequence 35, Appli
Sequence 35, Appli
Sequence 35, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 113, Appli
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14, Appl
6, Appli
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8, Appli
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                                                                                        (without alignments)
1.021 Million cell updates/sec
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                                                                            February 27, 2002, 11:36:03; Search time 132.19 Seconds
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-906-769-113
US-08-906-616-113
US-08-817-795-113
US-08-639-075A-113
US-09-012-431-113
US-09-012-692-113
US-08-906-613-113
US-08-991-813-1
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US-08-079-051-2
US-08-079-10-3
US-08-829-110-3
US-08-829-110-3
US-08-118-270-35
PCT-US93-08528-35
US-08-458-970A-9
US-09-082-310-1
                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-143-438-6
                                                                                                                                                                                                                       212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries
                                                   OM protein - protein search, using sw model
                                                                                                                                                                                               Gapop 10.0 , Gapext 0.5
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                                                                                                                      US-09-446-109A-7
                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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                                                                                                                      Title:
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                                                      US-09-413-814-10
US-09-091-219-25
US-09-091-219-2
US-08-704-655-20
US-08-665-543B-4
US-08-766-858A-27
US-09-164-193-8
US-08-997-080-75
US-08-997-080-75
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US-08-997-362-194
US-09-095-855-194
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US-09-095-855-75
US-09-334-601-13
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ALIGNMENTS

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OTHER INFORMATION: /label= BH
OTHER INFORMATION: /note= "either the natural phenylalanine amino
OTHER INFORMATION: terminus or the Bolton-Hunter modified peptide
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,137
                                                                                                                       Sirth.
SITY: Rahway
SITY: New Jersey
OninTRY: United States of America
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GENERAL INFORMATION:
APPLICANT: MORGAN, EDWARD L.
APPLICANT: EMBER, JULIA A.
APPLICANT: HUGLI, TONY E.
TITLE OF INVENTION: ANTIBODIES TO HUMAN C5a RECEPTOR NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/079,051
FILING DATE: 18-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John W.
REFERENCE/DOCKET NUMBER: PD-2790
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                             ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los.Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application PC/TUS9406994 GENERAL INFORMATION:
                                                                                                                            Sequence 2, Application US/08079051
Patent No. 5480974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO. 2.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 16 amino acids
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CLONE: C5aR(133-148)
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Best Local Similarity
Matches 4; Conserv
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7 FKPIW 11
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; LOCATION:
US-08-079-051-2
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DCT-US94-06994-2
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US-08-079-051-2
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OTHER INFORMATION: having the group 3-(p-hydroxypenyl)propionyl group
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                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Tajlor, Robert
APPLICANT: Erfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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Pred. No. 8.3;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                            Length 6;
                                                        LOCATION: 4
COTHER INFORMATION: /label-dcha
OTHER INFORMATION: /note-"D-cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: VS-040G-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                        94.3%; Score 33; DB 1; L
100.0%; Pred. No. 1.6e+05;
ive 0; Mismatches 0;
                                                                                                                                                                          ; OTHER INFORMATION: /label= darg
; OTHER INFORMATION: /note= "D-arginine"
US-08-215-137-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604tenburg Ph.D., Carol
RECISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 26, Application US/08915314
; Patent No. 6180604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7%;
Matches 4: Conservative
                                                                                                                                       NAME/KEY: Modified-site
LOCATION: 6
                                        NAME/KEY: Modified-site
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LENGTH: 13 amino acids
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Best Local Similarity 100.
Matches 6; Conservative
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US-08-915-314-26
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US-08-915-314-26
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80.0%; Score 28; DB 1; Length 16; 80.0%; Pred. No. 10;
                                           1; Indels
                                                                                                                                                                                                                                                                            APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: ANTIBODIES TO HUMAN C5a RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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Score 28; DB 3; Length 115; Pred. No. 72;
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Patent No. 5882890
GENERAL INFORMATION:
APPLICANT: GILL SULYA K.
TITLE OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
TITLE OF INVENTION: SIGNALING
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CTTY: Palo Alto
                                                                                                    PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 7-007177

FILING DATE: 20-JAN-1995

PROR APPLICATION NUMBER: JP 6-7-7

APPLICATION NUMBER: JP 6-7-7

FILING DATE: JP 6-7-7

PRIOR APPLICATION NUMBER: JP 6-7-7
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JF 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
                                              FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
SILING DATE: 16-MAR-1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-ANG-1945
PRIOR APPLICATION DATA: JP 6-189272
APPLICATION NUMBER: JP 6-189272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.08;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Resnick, David S. REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 617-523-6440 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                    FILING DATE: 10-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-513-974B-351
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4 FKPIW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IS-08-829-110-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN, TITLE OF INVENTION: PRODUCTION, AND USE THEREOF NUMBER OF SEQUENCES: 380 CORRESPONDENCE ADDRESS: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP STREET: 130 Water Street
                             COUPUTER EACACHELE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Plan PC COMPATIBLE
COREMATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC-194
CLEASIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Tumarkin, Lisa A.
REGISTRATION NUMBER: PC-190
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
TELEFONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARRACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-5EP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 351, Application US/08513974BPatent No. 6114139GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Gujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shojii
APPLICANT: Ohgi, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: C5aR(133-148)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide
LOCATION: 1..16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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7 FKPIW 11
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US-08-513-9748-351
                    9006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MA
COUNTRY: L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FKPXW 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION:
PCT-US94-06994-2
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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FEGURATION PC/TUS9308528
Sequence 35, Application PC/TUS9308528
GENERAL INFORMATION:
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                     Score 28; DB 1; Length Jure Pred. No. 1.98+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 5; Length 304
Pred. No. 1.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patchtln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MURPHY=2 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: MURPHY=2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34,033
            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 248633
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                      80.0%;
80.0%;
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Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                      TELEX: 248633
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 amino acids
                                                                                                                                                                                                                                                                                                                                                 4; Conservative
                                                                                                                                                                                  single
                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-118-270-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                               103 FKPIW 107
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                                                                                                                                                                                                                                                                                                                                                                                     1 FKPXW 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US93-08528-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB 2; Length 243;
Pred. No. 1.5e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFWHARE: Patentin Release #1.0, Version #1.25 SOFWHARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270 FILIGO DATE: 09-5EP-1993 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236 FILIGO DATE: 10-5EP-1992 ATTORNEY/AGENT INFORMATION:
                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,110
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PROR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOAPY disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Sequence 35, Application US/08118270
: Patent No. 5508384
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 243 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLCGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 415-855-0555
TELEFAX: 412-845-4166
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Townsend, Kevin G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
      ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THYMNOT02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LIBRARY: THYM); CLONE: 343504
US-08-829-110-3
                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 KPAWR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KPXWR 6
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Score 28; DB 3; Length 463; Pred. No. 2.9e+02; 0; Mismatches 1; Indels
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APPLICANT: **.mar, Chandrika
APPLICANT: **.drau, Herry
TITLE OF :**VENTION: THERAPEUTIC AND SCREENING
TITLE OF :**VENTION: METHODS USING C3A RECEPTOR AND C3A
NUMBER OF ***NCES: 5
                                                                                                                                                SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,310
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
SUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,874
                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0520 US
TELECOMUNICATION INFORMATION:
TELECHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08876874 Patent No. 5942405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF "NCES: 5
CORRESPONDED ADDRESS:
ADDRESSEN: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.08;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.v.
A. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bergsma, Derk
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APPLICANT: Ames, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
                  CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
PALO ALTO
                                                                                                                                                                                                             FILING DATE: H
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; CLONE: 2124957
US-09-082-310-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PESULT 11
US-08-876-874-2
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                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
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Patent No. 6096256
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: HUG, Henry
TITLE OF INVENTION: HUMAN NUCLEIC ACID METHYLASES
                                                                                                            Sequence 9, Application US/08458970A
Patent No. 5861272
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF: INVENTION: C5a Receptor
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: CEARELLA BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART 6 OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28; 'DB 2; I Pred. No. 2.2e+02; 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/458,970A FILING DATE: June 2, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US94/09234 FILING DATE: 16 AUG 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    325800-353
                                                                                                                                                                                                                                                                                                                                                              ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AUGUS.
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-11700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
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; MOLECULE TYPE: protein
US-08-458-970A-9
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CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PH
                                                                                                                                                                                                                                                                             STREET: 6 BECREN CITY: ROSELAND STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 FKPIW 143
111 |
103 FKPIW 107
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                                                                            RESULT 9
US-08-458-970A-9
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Gaps
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APPLICANT: Rushlow, Keith E. APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R. APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Patrick J. APPLICANT: Glines, Patrick J. APPLICANT: Gliver, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF CORRESPONDENCE: 190
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0
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Pred. No. 3.1e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2-3
TELECOMMUNICATION INFORMATION:
TELEFHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 113:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/906,616 FILING DATE: 05-ANG-1997 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Sequence 113, Application US/08906616 Patent No. 6121035 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 113, Application US/08817795 Patent No. 6139840
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80.0%;
                                                                                          Query Match 80.0%;
Best Local Similarity 80.0%;
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 496 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
35-08-906-616-113
         ; MOLECULE TYPE: protein US-08-906-769-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 80203
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Denver
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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358 FKPKW 362
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358 FKPKW 362
                                                                                                                                                                                   1 FKPXW 5
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                                                                                                                                                                                                                                                                                                                  US-08-906-616-113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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Pred. No. 3e+02;
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APPLICANT: Rushlow, Keith E.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Friedies, Patrick J.
APPLICANT: Silegier, Gary
APPLICANT: Silver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 80203
ZIP: 80203
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24 - APR-1996
ATTORNEY/AGENT IRFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEFONE: (303) 863-9700
TELEFONE: (303) 863-9700
TELEFONE: (303) 863-0223
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P50501
TELECOMNUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 113, Application US/08906769; Patent No. 6077687; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            80.0%;
80.0%;
                                                                                                                                                   TELEX: 846169
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 482 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
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HOLECULE TYPE: protein
US-08-876-874-2
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| 125 FKPIW 129
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CITY: Denve
STATE: Color
COUNTRY: US
ZIP: 80203
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                                                                              APPLICANT: Heath, Andrew W.
APPLICANT: Yamaka, Miles Yamanaka
APPLICANT: Arfsten, Anies Yamanaka
APPLICANT: Steed-er, Gary
APPLICANT: Steed-er, Gary
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: NEED OF PROTEASE TO PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: INFESTATION, AND FLEA PROTEASE PROTEINS, NUCLEIC ACID
NUMBER OF SEQUENCES: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLEA PROTEASE PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                    STATE: COLORAdo
COUNTRY: USA
ZUP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 113, Application US/08639075A
Patent No. 6150125
GENERAL INFORMATION:
APPLICANT: Grieve, Robert B.
APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Sliver, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Gary J. Connell
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 7.020
TELECOMMUNICATION INFORMATION:
TELECHONE: (303) 863-9700
TELEFAX: (303) 863-9223
INFORMATION FOR SEO ID NO: 113: SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                                         Hunter, Shirley Wu
Frank, Glenn R.
Grieve, Robert B.
Rushlow, Keith E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SILVEr, GARY
TITLE OF INVENTION: FLEA
TITLE OF INVENTION: MOLE
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein US-08-817-795-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         Denver
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358 FKPKW 362
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                                                          APPLICANT:
APPLICANT:
APPLICANT:
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Length 496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 4; 1
Pred. No. 3.1e+02;
0; Mismatches 1;
                                        STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-25-C2
TELECOMMUNICATION INFORMATION:
TELEFAX: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 27, 2002, ii:36:04 Job time: 143 sec
                      Sheridan Ross & McIntosh
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                    Colorado
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Peptide #8203 cnco Peptide #12130 enc Arabidopsis thalia Arabidopsis thalia Peptide #3326 enco Peptide #3347 enco Peptide #3347 enco

Human gastric canc -deoxy-D-xylulose

AAM29310 AAM04538 AAB63599

AAG60383 AAM16826

AAM21769

AAR37

AAM38093

AAG56373

AAR64890

Zea mays protein Zea mays protein Zea mays protein Zea mays protein f Anti-adipocyte mon Human secreted pro Arabidopsis thalia Zea mays protein f

ALIGNMENTS

(first entry)

AAG10416

AAG03617 AAC40668

lea mays protein f

Human ORFX ORF238

AAG27126 AAB40474

AAG26786 AAG26045

AAB01365 AAG40669

AAG19056

Indolicidin analog Indolicidin analog Indolicidin analog Cationic peptide o

Human colon cancer Human protein sequ Human neuron proge

Newcast, le disease

AAK51233 AAB53989

AAB93531

Amino acid sequenc Amino acid sequenc Amino acid sequenc Human C5a receptor Chemoattractant C5

816 853 854

AAY91

AAY91 AAY91

AAW66370

AAW66371 AAW66377

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Anaphylatoxin: receptor; ligand; antiinflammatory; hexapeptide; hagh-apeptide; immunodeficiency; allergy; autoimmune; ARDS; cancer; haff-stion; endotoxin; asthma; gout; psoriasis; cirrhosis; nitiammatory; bowel; discase; hepatitis; burns; myocardial; infarction; transplant rejection; ischaemic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anaphylatoxin antagonist or agonist peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR 30577 standard; peptide: 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-1993
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AAR30577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
AAR30577
 (without alignments)
1.464 Million cell updates/sec
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                                                                                                                                 February 27, 2002, 11:41:15; Search time 303.5 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A_ceneseq_1101:

/ SIDSB/gcqdata/qeneseqp/AA1980.DAT:

/ SIDSB/gcqdata/qeneseqp/AA1981.DAT:

/ SIDSB/gcqdata/qeneseq/qeneseqp/AA1981.DAT:

/ SIDSB/gcqdata/qeneseq/qeneseqp/AA1982.DAT:

/ SIDSB/gcqdata/qeneseq/qeneseqp/AA1981.DAT:

/ SIDSB/gcqdata/qeneseq/qeneseqp/AA1991.DAT:

/ SIDSB/gcqdata/qeneseq/qeneseqp/AA1991.DAT:
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                            522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
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Maximum Match 100%
Listing first 45 summaries

    prolein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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                                                                                               OM protein
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9
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"(2R)-2-amino-3-cyclohexyl-propanoyl" Location/Qualifiers /note= "N-Me-Phe" "D-Arg' /label-, OTHER 91WO-US09319 90US-0634641 /note= /note= Koy Modified-site Modified-site Mod_fied-site 1.3-10PC-1991; 27 - DBC - 1990; 439211858-A 21-JUL-1992 Corn putalization of Veast G protein-co Yeast G protein-co Anaphylatoxin anta CSa peptide analog Human D2H binding

AABD1208 AAC98875 AAY58359 AAY58360 AAY58358 AAY58356 AAY58356

434 462 700 847 864 953 953

85.7 85.7 85.7 85.7 85.7 85.7

13 16 20 21 22 21 21 21 21 21 21 21

AAR89737 AAW74031

AAR30577

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us-09-446-109a-8.rag

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Claim 2; Page 54; 294pp; English
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                                Konteatis Z,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WQ9851325-A2
                                                                                                                                                                                                                                                                                                   1 fkpxwr
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                                                                                                                                                                                                                                                                                                                                                                     AAW74031;
                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                           Matches
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                                                                                                                         The peptide is a specifically claimed example of a group of highly generic hexa- and heptapeptides which are (a) anaphylatoxin antagonists useful for tracting asthma, other allergies, inflammations, autoimmune diseases, serum sickness, gout, bullous skin diseases, psoriasis, ANDS, endocoxin shock, hepatic cirrhosis pancreatitis, inflammatory bowel disease, burns, sepsis, myocardial infarction, chronic hepatitis, transplant rejection, or ischaemic heart or brain damages or (b) anaphylatoxin agonists useful for stimulating inflammatory and immune responses, e.g. in the treatment of cancer, immunodeliciency diseases and severe infections.
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         C5a; complement; agonist; antagonist; peptide; binding assay; identification; inflammation; pain reduction; respiratory disorder; cardiovascular; hypertension; ARDS; anaphylaxis; arthritis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /labc!- Phc, OTHER /note- "OTHER - the Bolton-Hunter modified peptide having the 3-(p-hydroxyphenyl)-propionyl
                                                                   New hexar and hepta:peptide(s) are anaphylatoxin antagonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                      C5a peptide analoque, C089, used to identify C5a (ant)agonists.
                                                                                                                                                                                                                                                                                        0;
                                                                              agonists - for treating inflammatory and immunodeficiency diseases, cancers and severe infections
                                                                                                                                                                                                                                                                      Length 6;
                                                                                                                                                                                                                                                                                       Indels
                              Wagner R, Wiedeman PE;
                                                                                                                                                                                                                                                                   94.3%; Score 33; DB 13; 1100.0%; Pred. No. 4.3e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /noter "O-cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "cyclohexylalanine"
                                                                                                         Claim 11; Page 153; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                            AAR89737 standard; peptide; 6 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label - OTHER
          (ABBO ) ABHOTT LABORATORIES
                              Or YS,
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                                WPI; 1992-268383/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 4
                                                                                                                                                                                                                                      6 AA;
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Misc-difference
                                                                                                                                                                                                                                                                                                          1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     competitive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                       Sequence
                            Kawai M,
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AAR89737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Castro-intestinal transport receptor; bindiny protein; hSI; HPPI; pDIII hepPI; human; GI Lrack receptor; sucrose-isomaliase complex; intestinal peptide-associated transporter; hyperlension; diabetes; osteoporosis; haemophilia; anaemia; cancer; migralne; angina pectoris;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ö
                                                                                                                                                                                        C5a receptor binding assays - used for identifying cpds.having C5a antagonist, agonist or partial agonist activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimaeras and antibodies, used to deliver therapeutic or diagnostic agents to, through, the gastrointestinal tract, e.g. insulin or leuprolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; L. 4.3e+05;
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O
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                                                                     Springer MS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW74031 standard; peptide; 39 AA.
                                                                                                                                                                                                                                                                                 Claim 15; Page 47; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human D2H binding protein DAB3.
                                                              Siciliano SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US10088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
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(MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ELAN-) ELAN CORP PLC.
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                                                                                                                             WPI; 1995-344718/44.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA;
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This sequence represents a peptide that specifically binds to the human 1924 protein. The invention relates to purified proteins (1) that bind specifically to at least one of the gasto-intestinal (6) tract creeptors human intestinal peptide associated transporter (HPT).

Treeptors human sucrose-isomaltase complex (hSI). (1) provide active transport of therapeutic agents through human and animal GI tissue (1 into the blood) for in vivo delivery, particularly for treatment or prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia, cancer, imajraine, or amijna pectoris. Specifically thry are used to deliver insulin or leuprolide, but many other suitable therapeutic agents are disclosed, including genes or inhibitory nucleic acid, imaging agents and antigens. (1) may also provide targeting to the GI tract. Other uses of (1) are: (1) to determine the level of specified receptors in a sample (1) are: (1) to determine the level of specified receptors in a sample (1) are: (1) to many other suitable therapeutic analogues or derivatives of (1) are used to raise antibodies and in immunoassays. The antibodies are used to locate, detect and measure (1), e.g. for imaging mondification.
×55666556666666666666666
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39 AA; Sequence

Gaps .; 0 Score 30; DB 20; Length 39; Pred. No. 18; 1; Indels 1; Mismatches 85.78; 66.78; 4; Conservative Best Local Similarity Query Match Matches

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1 FKPXWR 6

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15 frpgwr 20

AAB01208 standard; Protein; 434 AA. 12-DEC-2000 AAB01208; . RESULT AAB01208

(first cntry)

Corn putative lecithin:cholesterol acyltransferase #3.

Corn; lecithin:cholesterol acyltransferase; phytosterol; phosphatidylcholine-sterol O-acyltransferase; heat shock; cold shock

Zea mays.

WO200032791-A2.

08-JUN-2000

99WO-US28586. 02-DEC-1999;

98US-0110782. 03-DEC-1998; (DUPO) DU PONT DE NEMOURS & CO E 1..

Saylor JJ; Butler KH, Shen JB, Sakai H, Cahoon RE, Kinney AJ,

WPI; 2000-412337/35. N-PSDB; AAA49203

Polynucleotide encoding plant lecithin; cholesterol acyltransferase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries

Claim 10; Page 40-41; 49pp; English.

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The present sequence is a putative protein sequence of a corn lecitlinicholesterol acyltransferase (also known as phosphalidylcholine-sterol 0-acyltransferase). This enzyme is found associated with high-density lipoproteins and Apolipoprotein-Al and -D.
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childed DNA sequences (I). AANB4500 to AANB4670 encode the E. colinariated DNA sequences (I). AANB4500 to AANB4670 encode the E. colinariated DNA sequences (I). AANB4500 to AANB4670 encode the E. colinariated but and the proliferation related proteins given in AAA9907B and AAG98830 to AAG98999. (I) can be used as potential targets for the generation of encoded and the proteins and the generation of the proteins, the purified proteins can be used; to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed system compound libraries for compounds. In addition, nucleic acid probes system compound libraries for compounds. In addition, nucleic acid probes system or an be used to identify particular microorganism species of microorganisms can be used to identify particular microorganism species and information of libraries of providing a rapid and dependable of information and proliferation-required sequences can also be used a screen for specific microorganisms that produce such proteins in a screen for specific microorganisms that produce such proteins in a screen for specific microorganisms that produce such proteins in a screen for specific microorganisms that produce such proteins in a screen for sequencing processing sequencing processing sequencing processing sequencing processing sequencing and ease used in an example from the present. ö The gene and protein can be used to produce transgenic plants which have increased lipid metabolism and membrane fluidity, and therefore increased resistance to heat and/or cold shock, to alter the content of phytosterol or lecithin in grains and to identify potential herbicides. ebli growin and proliferation related protein sequence SEQ 1D NO:345. Movel nuclein acids that inhibit Escherichia coli proliferation, useful tor screening for homologous genes and for designing expression vectors Gaps Escherichia coli; growth; proliferation; microbial; antimicrobial; Pecterial infection; microorganism. . 0 Length 434; Score 30; DB 21; Length 43 Pred. No. 2.1e+02; 1; Mismatches 1; Indels Clarm 19; Page 421-422; 522pp; English. AAG98875 standard; Protein; 462 AA. Ohlsen K, Zyskind J; 85.7%; 66.7%; 09-NOV-2000; 2000WO-US30950 (lirst entry) Outry Match
Hesr Local Similarity 60...
4; Conservative (EL.T.) ELITRA PHARM INC WPI; 2001-335933/35 AA; Escherichia coli. N-PSDB; AAH84546 27: frpmwr 376 W0200134810-A2 ٠. 09-NOV-1999; 26 -SEP-2001 Forsyth RA, J. FKPXWR 7 - MAY - 2001 AAGS8875; Sequence 'n AAG98875 ò 8×6000

The invention relates to a novel yeast G protein-coupled receptor, C GPRI (AAY\$835). GPRI is predicted to have seven transmembrane domains, which is characteristic of G protein-coupled receptors, and also contains a very large third cytoplasmic loop and a large cytoplasmic tail. The third cytoplasmic loop contains two short basic sequences; one sequence (KRKRAOIG) is present at the N-terminal end of the loop and the chird cytoplasmic loop also contains an asparagine-rich region. GPRI is believed to provide the upstream signal that activates GPR2, and plays an essential role in inducting the switch from hor-filamentous to filamentous growth in yeast. Modulators of GPRI function, especially inhibitors, are useful for prevention or treatment of a disease or disorder involving a fungal infection. The inhibitor may be an anti-GPRI antibody, GPRI antisense nucleic acid or a GPRI quee altered so that an inserted heterologous sequence inactivates the biological activity of GPRI. Compounds which modulate GPRI gene expression and/or gene product activity may be used to inhibit the conversion of a fungus from a non-filamentous form to a filamentous form. The present sequence in the conversion of a fungus from a non-filamentous form to a filamentous form. The present sequence ö the invention. This sequence is lacking the majority of the cytoplasmic Creaminal tail, relative to the native GPRI. Note: This sequence is not shown in the specification, but is derived from the yeast GPRI amino acid sequence given in figure 1A. Gaps Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mutein. .; o Novel protein, gene, antibody and recombinant cell useful for identifying modulators and inhibitors useful as anti-fungals Score 30; DB 22; Length 462; Pred. No. 2.3e+02; 1; Mismatches 1; Indels Yeast G protein-coupled receptor GPR1 mutant d694-954. example 6.2.5; Page -; 63pp; English. (MOUN) MOUNT SINAI SCHOOL MEDICINE. AAY58359 standard; Protein; 700 AA. 85.78; 98US-0088311. 99WO-US11838 27-MAR-2000 (first entry) Ouery Match

Best Local Similarity 66.7

Matches 4: Conservative Saccharomyces cerevisiae WPI; 2000-086980/07. (irsch JP, Xue Y; 462 AA; 11 11 398 ykplwr 403 1 FKPXWR 6 28-MAY-1999; 01-JUN-1998; W09963094 - A2 09-DEC-1999. Synthetic. AAY58359; Sequence 9 AAY58359
AAY58359
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AAY AAY58359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel yeast C protein-coupled receptor, GPR1 (AAY58355). GPR1 is predicted to have seven transmembrane domains, which is characteristic of G protein-coupled receptors, and also contains a very large third cytoplasmic loop and a large cytoplasmic tail. The third cytoplasmic loop contains two short basic sequences; one sequence (KRIKAQIG) is present at the N-terminal end of the loop and the other sequence (KKRRAQIO) is at the C terminal end of the loop. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      third cytoplasmic loop also contains an asparagine rich region. GPRI is believed to provide the upstream signal that activates GPA2, and plays an assential role in inducing the switch from non-filamentous to filamentous growth in yeas. Modulators of GPRI function, especially inhibitors, are useful for prevention or treatment of a disease or disorder involving a fungal infection. The inhibitor may be an anti-GPRI antibody, GPRI antisense nucleic acid or a GPRI gene altered so that an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inserted heterologous sequence inactivates the biological activity of GPR1. Compounds which modulate GPR1 gene expression and/or gene product activity may be used to inhibit the conversion of a fungus from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This sequence is not shown in the specification, but is derived from the yeast GPRI amino acid sequence given in figure 1A.
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              represents a GPR mutant, d277-284, used in an exemplification of
the invention. This sequence is lacking a portion (designated the
SmaRest region) of the cytoplasmic C-terminal tail, relative to the
                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-filamentous form to a filamentous form. The present sequence
                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel protein, gene, antibody and recombinant cull useful for identifying modulators and inhibitors useful as anti-fungals
                                                        Score 30; DB 21; Length 700; Pred. No. 3.5e+02;
                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                            feast G protein-coupled receptor GPR1 mutant d841-954.
                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5.2.5; Page -; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                                                                        AAY58360 standard; Protein; 847 AA.
                                                      85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0088311.
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                          Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-086980/07.
700 AA;
                                                                                                                                                                        156 fkpnwk 161
                                                                                                                                   1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                     27-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               native GPR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
Sequence
                                                                                                                                                                                                                                                                                                               AAY58360;
                                                          Query Match
                                                                                                                                                                                                                                                     AAY58360
                                                                                                                                                                                                                                    RESULT
                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                          SXX
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847 AA;

Sequence

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The invention relates to a novel yeast G protein-coupled receptor.

CPRI (AAY$835). GPRI is predicted to have seven transmembrane domains, which is characteristic of G protein-coupled receptors, and also contains a very large third cytoplasmic loop and a large cytoplasmic sequences. The third cytoplasmic loop contains two short basic sequences: one sequence (KRKRAOIG) is present at the Y-terminal end of the loop and the other sequence (KRRRAOIG) is at the G-terminal end of the loop and the other sequence (KRRRAOIG) is at the G-terminal end of the loop. The third cytoplasmic loop also contains an asparagine-rich rogion. GPRI is believed to provide the upstream signal that activates GPA2, and plays an essential role in inducing the switch from non-filamentous to tilamentous growth in yeast. Modulators of GPRI function, especially inhibitors, are useful for prevention or treatment of a disease or disorder involving a fundal infection. The inhibitor may be an anti-GPRI antiscnsc nucleic acid or a GPRI genc altered so that an inserted heterologous sequence inactivates the biological activity of GPRI. Compounds which modulate GPRI genc expression and/or gene product activity may be used to inhibit the conversion of a fundus from a
                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represents a CPR mulant, d277-284, used in an exemplification of the invention. This sequence is lacking the asparagine-rich region of the third cytoplasmic loop, relative to the native GPRI. Note: This sequence is not shown in the specification, but is derived from the yeast GPRI amino acid sequence given in figure IA.
                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-filamentous form to a filamentous form. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protein, gene, antibody and recombinant cell useful for identifying modulators and inhibitors useful as anti-fungals
DB 21; Length 847;
Score 30; DB 21; Length 84
Pred. No. 4.2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                  Yeast G protein-coupled receptor GPR1 mutant d490-586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 6.2.5; Page -; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOUN ) MOUNT SINA! SCHOOL MEDICINE.
                                                                                                                                                                                                                         AAY58358 Standard; Protein; 864 AA.
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US11838
                                                                                                                                                                                                                                                                                                          (first cutry)
                     Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-086980/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hirsch JP, Xue Y;
                                                                                                         |||| |:
|156 fkpnwk 161
                                                                                  1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9963094-A2
                                                                                                                                                                                                                                                                                                          27-MAR-2000
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  Query Match
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contains a very large third cytopeamic loop and a large cytoplasmic contains a very large third cytopeamic loop and a large cytoplasmic contains two short basic sequences: one sequence (KRRAQIO) is present at the N-terminal end of the loop and the other sequence (KRRAQIO) is at the C-terminal end of the loop and the chird cytoplasmic loop also contains an asparagine-rich region. GPRI is believed to provide the upstream signal that activates GPA2 and plays an essential role in inducing the switch from non-filamentous to sequence in inducing the switch from non-filamentous countries. Modulators of GPRI function, especially inhibitors, are useful for prevention or treatment of a disease or disnoible involving a fungal infection. The inhibitor may be an anti-GPRI intended, GPRI antisease uncleic acid or a GPRI gene altered so that an inserted heterologous sequence inactivates the biological activity of size compounds which modulate GPRI gene expression and/or gene product activity may be used to inhibit the conversion of a fungus from a non-filamentous form to a filamentous form. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is invention. This sequence is lacking the first basic motif (KRIKAQIG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fire invention relates to a novel yeast G protein-coupled receptor, 1978; (AAY58355). GPRI is predicted to have seven transmembrane domains, which is characteristic of G protein-coupled receptors, and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the third cytoplasmic loop, relative to the native GPRI.

Whate: This sequence is not shown in the specification, but is derived from the yeast GPRI amino acid sequence given in figure 1A.
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Yeast, G protein-coupled receptor, GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     represents a GPR mutant, d277-284, used in an exemplification of
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Movel protein, gene, antibody and recombinant cell useful for identifying modulators and inhibitors useful as anti-fungals
  Length 864;
                                          Indels
                                                                                                                                                                                                                                                                                                                                                  reast G protein-coupled receptor GPR1 mutant d277-284.
                                        ä
Score 30; DB 21;
Pred. No. 4.3e+02;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                                           AAY58356 standard; Protein; 953 AA.
n 85.7%;
Similarity 66.7%;
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0088311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sarcharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4P.I.: 2000-085980/07
    Query Match
Bess Local Similarity
Matones 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hirsch JP, Xue Y;
                                                                                                         L FKPXWR 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09963094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38-MAY-1994
                                                                                                                                                                                                                                                                                                         27-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synchetic
                                                                                                                                                                                                                                                                   AAY58356;
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                                                                                                                                                                                                          AAY58356
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Score 30; DB 21; Length 953; Pred. No. 4.7e+02;

85.7%;

Best cosal Similarity

Que 17 Match

864 AA;

sednence

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156 fkpnwk 161
   1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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                                                                                                    AAY58355
ID AAYS
                                  qo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a movel yeast G protein-coupled receptor, C CPRI (AAYS035). GPRI is predicted to have seven transmembrane domains, which is characteristic of G protein-coupled receptors, and also contains a very large third cytoplasmic loop and a large cytoplasmic loop contains two short basic sequences; one sequence (KRIKAOIG) is present at the N-terminal end of the loop and the collect sequence (KRIKAOIG) is at the C-terminal end of the loop and the third cytoplasmic loop as contains an asparagine-rich region. GPRI is believed to provide the upstream signal that activates GPA2, and plays an essential role in inducing the switch from non-filamentous to filamentous growth in yeast. Modulators of GPRI function, especially inhibitors, are useful for prevention or trealment of a disease or disorder involving a fungal infection. The inhibitor may be an anti-GPRI antibacky, GPRI antisense muchaics acid or a GPRI gene altered so that an inserted hoteerologous sequence inactivates the biological activity of contility may be used to inhibit the conversion of a fungus from a conversion of a fungus from a conversion of a fungus from a
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   Gaps
                                                                                                                                                                                                                                                                                         Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-filamentous form to a filamentous form. The present sequence represents a GPR mutant, d610-617, used in an exemplification of the invention. This sequence is lacking the second basic motif
 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel protein, gene, antibody and recombinant cell useful for identifying modulators and inhibitors useful as anti-fungals
 Indels
                                                                                                                                                                                                                                                         Yeast G protein-coupled receptor GPR1 mutant d610-617.
 1;
 Mismalches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6.2.5; Page -; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                  AAY58357 standard; Protein; 953 AA.
 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US11838
                                                                                                                                                                                                            27-MAR-2000 (Lirst entry)
                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.
4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-086980/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               953 AA;
                                                   111 1:
156 fkpnwk 161
                                1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                      AAY58357:
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                                                                                                                  RESULT 10
Matches
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filamentous growth;
                                                                  Yeast; G protein-coupled receptor; GPR1; filamentc
pseudohyphal form; signalling pathway; antifungal.
                                                                                                                                                                                                                                                                                                                                                                     /note= "Basic motif 2 (KKRRAQIQ)"
621..645
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Intracellular C-terminus"
                                                                                                                                                                                                                                                                                                                          277..284
/notc= "Basic motif 1 (KRIKAQIG)"
                                                                                                                           /note= "Extracellular N-terminus"
                                                                                                                                                                                                                                                                                                                                                     /note= "Asparayine-rich region"
                                                                                                                                                                                                                                                                                                                                                                                       "Transmembrane domain 6"
                                                                                                                                                                                                                                                                                                                                                                                                                        "Transmembrane domain 7"
                                                                                                                                            'note= "Transmembrane domain 1"
                                                                                                                                                                                                                                                                                   /note= "Transmembrane domain 5"
                                                                                                                                                                                                                domain 3"
                                                                                                                                                                             "Transmembrane domain 2"
                                                                                                                                                                                                                                                "Transmembrane domain 4"
                                                                                                                                                                           ..656
:e- "Extracellular loop 3"
                                                                                                                                                                                                                                                                 /note= "Extracellular Loop 2"
247..276
                                                                                                                                                                                                                                                                                                                   "Intracellular Loop 3"
                                                                                                                                                                                                                                /note= "Intracellular loop 2"
                                                                                                                                                                                                                                                                                                 /note= "Encoded by AGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by AGC"
                                                  feast G protein-coupled receptor GPRI.
                                                                                                                                                             'note= "Intracellular
                                                                                                                                                                                                               "Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOUN ) MOUNT SINAL SCHOOL MEDICINE.
                                                                                                            Location/Qualifiers
AAY58355 standard; Protein; 961 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-US11838
                                  (first entry)
                                                                                                                                                                                                               /note= "T;
157..180
                                                                                                                                                                                                                                                /note= "T
201..246
                                                                                                                                                                                                                                                                                                                                           .586
                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "T
679..961
                                                                                                                                                                                                                                         .200
                                                                                           Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                           277..620
                                                                                                                                                                                                                                                                                                                                                            610..617
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                                                                                                                                    56..80
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                                 27-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-DEC-1999
                AAY58355;
                                                                                                            Key
Region
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0

Gaps

0;

85.7%; Score 30; DB 21; Length 953; 66.7%; Pred. No. 4.7e102; Live 1; Mismatches 1: Indels

4; Conservative

Matches

Query Match Hest Local Similarity ö

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W.1; 2000-106102/09.
WPI; 1993-288410/36
                                                                                                                              1093 AA;
                                                                                                                                                                                                                                      387
                                                                                                                                                                                                                                                                                                                                                                                                                  ocal immunity.
                                                                                                                                                                                                              · 1 FKPXWR 6
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382 frprwr
                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                      AAY51233;
                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                       RESULT 13
                       DNA
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 ò
                                                                                                    This sequence represents a novel yeast G protein coupled receptor,

GPRI, GPRI is predicted to have seven transmembrane domains,
which is characteristic of G protein coupled receptors, and also
contains a Very large thic cytoplasmic loop and a large cytoplasmic

Lail. The third cytoplasmic loop contains two short basic sequences; one
sequence (KRRRAOIO) is present at the N-terminal end of the loop and the
other sequence (KRRRAOIO) is at the C-terminal end of the loop and the
cother sequence (KRRRAOIO) is at the C-terminal end of the loop. The
third cytoplasmic loop also contains an asparagine-rich region. GPRI is
believed to provide the upstream signal that activates GPA2 and plays
an essential role in inducing the switch from non-filamentous to
filamentous growth in yeast. Modulalors of GPRI function, especially
inhibitors, are useful for prevention or treatment of a disease or
disorder involving a fungal infection. The inhibitor may be an anti-GPRI
antibody, GPRI antisense nucleic acid or a GPRI gene altered so that an
inserted heterologous sequence inactivates the biological activity of
cPRI. Compounds which modulate GPRI gene expression and/or gene product
cother sequence involving a contained to inhibit the conversion of a fungus from a
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                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/note= "encoded by predicted reading frame a,
x's in the sequence indicate stop codons
in the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                          ;;
0
                                               protein, gene, antibody and recombinant cell useful for
                                                           identifying modulators and inhibitors useful as anti-fungals
                                                                                                                                                                                                                                                                                                                                                                  Score 30; DB 21; Length 961; Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abnormality; muscular dystrophy; CHR 19; chromosome 19; protein kinase; polymerase chain reaction; brain.
                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                          non-filamentous form to a filamentous form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human myotonin dystrophy gene protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR41001 standard; Protein; 1093 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                 Claim 4; Fig 1A; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                   85.7%;
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                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 66.7
Matches 4; Conservative
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           2000-086980/07
                                                                                                                                                                                                                                                                                                                                 961 AA;
                        N-PSDH: AA255699
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|156 Ekpnwk 161
                                                                                                                                                                                                                                                                                                                                                                                                                  1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FER-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lomo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR41001;
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comprises a rucleic acid sequence corresponding to the 5' Lerminal comprises a rucleic acid sequence corresponding to the 5' Lerminal end of the genome of avian-paramyxovirus allowing the generation of an infectious copy of avian-paramyxovirus. The cell line is useful for the productions copy of avian-paramyxovirus. The cell line is useful for the production of infectious lentogenic Nuv (Newcastle Discase virus) of a production of exagenous proteolytic activity. Also it is possible to generate a stable transfected cell line that expresses the viral discase of a production of exagenous proteolytic activity. Also it is possible to generate a stable transfected cell line that expresses the viral discase. Now can be easily cultured a stable form of a vaccine, especially adainst.

Crespiratory and/or gastrointestinal diseases. Now can be easily cultured an order of superior is relatively definite steed by mass application methods e.g. drinking water or he expraying or by aerosol formation. The natural route of infection is by an erosity formation. The natural route are also the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New avian paramyxovirus cDNA, useful for production of vaccine against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Avian-paramyxovirus; infection; lentogenic; F protein; vaccine; respiratory disease; gastrointestinal disease; poultry pathogen;
sequence of myotonic dystrophy gene - used to produce probes identify CHR 19 abnormality and protein kinase responsible
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                                                                                                                                                                                                            of
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1093;
                                                                                                                                                                                               The sequence is that encoded by predicted reading frame a the human myotonic dystrophy (DM) gene. It may be used in identification of individuals affected by DM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newcastle disease virus LaSota genome encoded protein 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 14; L. Pred. No. 5.5e+02; L. Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY51233 standard; Protein; 2204 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 visclosure; Fig 3; 115pp; English.
                                                                                                                               Disclosure; Fig 6; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-NL00377
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Matches 4; Conservative
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Gaps

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1; Mismatches

67;

Score 29; Pred. No.

82.9%;

90 AA;

DB 21; Length 90; 1; Indels

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Best Local Similarity 66.7
Matches 4; Conservative
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     invention
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routes of infection of many other poultry pathogens. NDV can induce local immunity despite the presence of circulating maternal antibody. This sequence represents a protein encoded by the NDV strain LaSota genome which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 called human colon cancer antigens, given in AAB3324 to AAB5406. The human colon cancer antigens, given in AAB3324 to AAB54066. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprolective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antinfective and antibacterial activities, and proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosts to the proteins are useful for the prevention, treatment and diagnosts of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent discases such as neural disorders, immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              system disorders, muscular disorders, reproductive disorders, quastrointecstimal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders, AAC99764 to AAC9772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colon cancer associated gene sequences, referred to as colon cancer antiqens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC97991 to AAC98763 encode the human colon cancer associated proteins,
                                                                                                                                                                                                                                                                                                                                                                             Human; colon cancer; colon cancer antigen; diagnosis; detection; Identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; qene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder;
                                                                                                                                          Gaps
                                                                                                                                         o;
                                                                                                             Score 30; 08 21; Length 2204;
Pred. No. 1.1e+03;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                     Numan colon cancer antigen protein sequence SEQ ID NO:1529.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infectious disease; cardiovascular disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 2083-2084; 2104pp; English.
                                                                                                                                                                                                                                                                  AAB53989 standard; Protein; 90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
                                                                                                             85.78;
66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                          Best Local Similarity 66.7
Matches 4; Conservative
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                                                                    2204 AA
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                                                                                                                                                                   1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-2000.
                                                                       Sequence
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                                                                                                               Query Match
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the specification. The primer sets can be used in an issense therapy and in gene therapy. The primer sets can be used in an issense therapy and in gene therapy. The primers are useful for synthesising polynucleolides, particularly full-length const. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length const. The primers allow obtaining of the full-length const. The primers allow obtaining of the full-length const. Anil 3538 and AAII 3633 to AAII 3642 represent human const sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sailo K, Yā
, Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ 1D NO:12886.
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Wakamatsu A,
                                                                                                                                                                                                                       AAB93531 standard; Protein; 217 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
22-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000; 2000EP-0316126
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                                                                                                                                                                                                                                                                                                                                                                             26-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPT; 2001-318749/34.
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111 |:
74 fkpcwk 79
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Ishii S, (
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AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention. 88888 88888

Sequence 217 AA;

0; 0; Gaps Ouery Match 82.9%; Scorc 29; DB 22; Length 217; Best Local Similarity 80.0%; Pred. No. 1.7e+02; Matches 4; Conservative 0; Mismatches 1; Indels

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Scarch completed: February 27, 2002, 11:41:15 Job time: 454 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein scarch, using sw model

February 27, 2002, 11:45:19; Search time 145.23 Seconds (without alignments) 3.147 Million cell updates/sec Kun on:

US-09-446-109A-8 1 FKPXWR 6 Title: Perfect scorum Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched: 219241 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* P1R_68:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	. formate hydrogenly	hypothetical 47.4	probable temA prot.	hypothetical prote	peptide transport	probable maturase	hypothetical prote	hypothetical 47.5	probable amino aci	conserved hypothet	hypothetical prote	probable membrane	G protein-coupled	genome polyprotein	hypothetical prote	yedG protein - Esc		hypothetical prote	LPS biosynthesis R	hypothetical prote	protein F2D10.28 (conserved hypothet	amino acid permeas	nodulation competi	hypothetical prote	hypothetical prote	probable glucose-6	glutamatecystein	carboxylesterase (
SUMMARIES	<u> </u>	C64364	E65146	1171279	н86020	T18250	878199	H72667	E65131	B86002	н69805	T31640	867568	JC5808	RRNZNV	T36433	H64956	F85810	1124993	1169147	1175484	C86340	H82504	T15052	A59268	G72753	877373	B82967	TU5142	534607
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عو	Ouery	94.3	94.3	94.3	94.3	94.3	9.88	85.7	85.7	85.7	85.7	85.7	85.7	85.7	85.7	8.5.9	82.9	82.9	82.9	85.6	82.9	82.9	82.9	82.9	82.9	82.9	82.9		82.9	82.9
	Score	33	33	33	33	33	31	30	30	30	30	30	30	30	30	29	58	29	56	53	50	29	29	29	29	5.6	29	53	29	53
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32 29 82.9 557 2 T39308 32 29 82.9 655 2 T30044 33 29 82.9 732 2 T50143 34 29 82.9 1224 2 255552 35 28 30.0 84 2 T48944 37 28 80.0 174 2 D86400 37 28 80.0 174 2 D86400 39 80.0 227 2 B70438 41 28 40.0 254 2 S10929 42 28 80.0 254 2 A49895 43 28 80.0 273 2 T3841 44 28 80.0 275 2 J50183 45 28 80.0 273 2 J50183	asparagine synthas	hypothetical prote	pumilio family pro	gene cob intron 3	hypothetical prote		envelope protein E	transposase - Myco	transposase - Flav	probable transloca	chitinase (EC 3.2.	hypothetical prote				
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		 .~	3.5	3.5	34	ic.	36	3.7	Ξ.	~	7	4.1	4.5	4.3	4	4.5

ALIGNMENTS

ormate hydrogen yase, subunit 5 -

RESULT

cus jannaschii

C;Species: Methanococcus jannaschil C;Date: 73-Sep-1936 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000 C;Accession: C64364

Religh, C.1.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak Religh, C.1.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, Tson, J.D.; Sadow, P.M.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996
A.Autaore: Kaine, 3.P.; Borodovsky, M.; Klenk, H.P.; Frascr, C.M.; Smith, H.O.; Woose A.Title: Jomplete genome sequence of the methanogenic archaeon, Methanococcus jannasc A.Reference number: A64300; MUID:96337999
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A.References: G81067501; GB:L77117; NID:92826289; PIDN:AAD98504.1; PID:q1591218
C.Gonz.List.

P; Man position: REV458767-457625

C.Superfamily: NAOH dehydrogenase (ubiquinone) 49K protein

0 Gaps .; 0 94.3%; Score 33; DB 2; Length 380; 83.3%; Pred. No. 27; ive 0; Mismatches 1; Indels Best Local Similarity 83.3 Matches 5, Conservative Query Match

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Applying the sal 47.4 kD protein in thsH-pit intergenic region - Escherichia coli (strain M.Alemhate names: hypothetical protein f409 c. Spaint: Escherichia coli (c. Spainter: Escherichia coli (c. Spainter: Escherichia coli (c. Spainter: E. Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-oct-1999 c. Accisson: E6546; S47710 P. Bloch, C.A.; Perna, N.T.; Burland, V.; Kiley, M.; A.; G.Se, D.J.; Aqu, B.; Shao, Y. A.; G.Se, D.J.; G.

£.Accidsion: E65146
A.Staris: nucleic acid sequence not shown; translation not shown,
A.NO.Staris type: DNA

EJRES diss: 1-412 <DLAT>
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Submisser to the SMBL Data Library, March 1994

11:23:41

Thu Feb 28

A:Reference number: S47666

Score 33; DB 2; Pred. No. 30; 0; Mismalches

Ouery Match, Best Local Similarity 83.3%; Matches 5; Conservative

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1 FKPXWR 6

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Albertied to the EMRL Data Library, August 1990
Albescription: The mitochondrial genome of the fission yeast Schizosaccharomyces pomb chizosaccharomyces pombe and Aspergillus nidulans.
Alreference number: $78195
Alreference number: $78195
Alreference number: $78195
Alreference number: $78196
Alreference number: $78196
Alreference: $781986
Alreference: $78196
Alref
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.Superfamily: cytochrome b6 homology; cytochrome b homology; plastoquinol--plastom; cytochrome iron: metalloprotein; mitochondrion
F.1-228/Region: cytochrome b exon 1 encoded
F.10-228/Jounain: cytochrome b homology #status atypical <CHH>
F:10-228/Jounain: cytochrome b6 homology CH65
F:222-228/Jounain: cytochrome b6 homology CH65
F:222-228/Jounain: cytochrome b6 homology ch65
F:229-1035/Region: cytochrome b intron encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide transport protein - yeast (Candida albicans)
C:Species: Candida albicans
C:Species: Candida albicans
C:Date.15-oct.1999 #sequence_revision 15-oct.1999 #Lext_change 15-oct.1999
C:Accession: T18250
R:Barrell, B.G.; Rajandream, M.A.
submitted to the BMBL Data Library, November 1998
A:Reference number: 218831
A:Reference number: 218831
A:Accession: T18250
A:Stelus: preliminary: translated from GB/EMBL/DDBJ
                                                                Gaps
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                                                           Indels
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                                                     Mismatches
          Pred. No. 40;
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Pred. No. 4
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A;Accession: S10070
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83.3%;
     83.3%;
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A;Residues: 1-1035 <LAW>
A;Cross-references: EMBL:X02819
                                           Conservative
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Best Local Similarity 83.3
Matches 5; Conservative
Best focal Similarity
Matches 5; Conserv
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A; Genetic code: SGC2
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A; Residues: 1-623 < HAR>
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189 FKPDWR 194
                                                                                                                                                 1 FKPXWR 6
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A:Introns: 475/3
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Science 281, 375-388, 1998
A.Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A.Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A.Status: proliminary; nucleic acid sequence not shown: translation not shown
A.Status: proliminary; nucleic acid sequence not shown: translation not shown
A.Status: 1-498 <a href="https://document.org/">A.Status: proliminary: nucleic acid sequence not shown: translation not shown
A.Status: 1-498 <a href="https://document.org/">A.Status: proliminary: nucleic acid sequence not shown: translation not shown
A.Status: 1-498 <a href="https://document.org/">A.Status: proliminary: nucleic acid sequence not shown: translation not shown
A.Status: 1-498 <a href="https://document.org/">A.Status: proliminary: nucleic acid sequence not shown: translation not shown
A.Status: 1-498 <a href="https://document.org/">A.Status: proliminary: nucleic acid sequence not shown: translation not shown
A.Status: 1-498 <a href="https://document.org/">A.Status: proliminary: nucleic acid sequence not shown: translation not shown
A.Status: 1-498 <a href="https://document.org/">A.Status: proliminary: nucleic acid sequence not shown: translation not shown
A.Status: 1-498 <a href="https://document.org/">A.Status: proliminary: nucleic acid sequence not shown: translation not shown
A.Status: 1-498 <a href="https://document.org/">A.Status: proliminary: nucleic acid sequence not shown: translation not shown
A.Status: 1-498 <a href="https://document.org/">A.Status: proliminary: nucleic acid sequence not shown: translation not shown
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A.Status: nucleic acid sequence not shown: translation not shown
A.Status: nucleic acid 
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Asture 409, 529-533, 201.
Asture 409, 529-533, 201.
Asture 400me sequence of enterohemorrhagic Escherichia coli 0157:H7.
A.Reference number: A85480: MUID:21074935; PMID:11206551
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A:Moldoule type: DNA
A:Moldoule type: DNA
A:Rosidues: 1-557 ckmp>
A:Cross-references: GB:AE005174: NID:912518181; PIDN:AAG58622.1; GSPDB:GN00145; UWGP:Z48
A:Experimental source: strain 0157:H7, substrain EDL933
A:Gene: Z4888
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G:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
G:Date: 24-Jul-1990 #sequence_revision 24-Jul-1990 #lext_change 05-Nov-1999
G:Accession: H71279
     A:Accession: S47710
A:Status: preliminary
A:Rolcoulc type: Dr. A:Residues: 1-394, MIJ.SRCFACS1' <PLU>
A:Residues: 1-394, MIJ.SRCFACS1' <PLU>
A:Residues: 1-394, MIJ.SRCFACS1' <PLU>
A:Cross-references: EMBL:U00039; NID:q466582; PIDN:AAB18466.1; PID:q466627
A:Robe: this sequence has been corrected
C:Genetics:
A:Gene: yhit.
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C.Dale: 16-Feb-2001 #sequence_revision 16-Feb-2001 #1.ext_change 31-Mar-2001
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94.3%; ilarity 83.3%; Conservative

Query Malch Best Local Similarity Matches 5; Conserv

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1 FKPXWR 6

C: Accession: B86020

A; Accession: B86020

Query Match

1; Mismatches

88.6%; 66.7%;

Best Local Similarity 66.7 Matches 4; Conservative

Query Match

111 1: 935 FKPSWK 940

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1 FKPXWR 6

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RKUNSEL, F.; Ogssawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber RKUNSEL, F.; Ogssawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron. S.; Bronillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter N.M.; A.; Elrikoth, S.D.; Errington, J.; Fabret, C.; Ferrari, Natur.; 340, 249-256, 1997
A.AULHOTS: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, A.; Galizzi, P.; Koninystein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau, W.; Mayara, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Ricqua, M.; Rivolta, C.; Rocha, R.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlakuri, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya, T.; Winders, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya, A.; Tunaka, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Yoshida, A.; Tillet, The complete genome sequence of the Gram-positive bacterium Bacillus subtili A. Retriescing number: Accession of the Gram-positive bacterium Bacillus subtili
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A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Crass-references: GB:AE005174; NID:g12517998; PIDN:AAG58478.1; GSPUB:GN00145; UMGP: A;Experimental source: strain 0157:H7, substrain EDL933 C;Genetics:
                                                                                                                                                                          Riberia, N.T.; Plankett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller. L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Polamousis, K.; Apoda Natura, 409, 529-533, 2001
Affilter. Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Refuence number: A85480; MUID:21074935; PMID:11206551
A; Accession: B86002
probable amino acid/amine transport protein yhfM [imported] - Escherichia coli (strai
C.Species: Escherichia coli
C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
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A:Residues: 1-606 <KUN>
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C.Datu: 05-Dec:1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
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Pred. No. 1.7e+02;
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Pred. No. 1.3e+02;
1; Mismatches 1; Indets
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Hilarity 66.7%;
Conservative
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Best Local Similarity
Matches 4; Conserv
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Best focal Similarity
Matthes 4, Conserv
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A;Molecule type: DNA
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398 YKPLWR 403
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                                                                                                                                     C; Accession: B86002
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Cispecles: Aeropyrum pernix
Cispecles: Airopyrum perni
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C;Superfamily: Methanobacterium thermoautotrophicum conserved hypothelical protein WTHIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AKO00413; GB:U00096; NID:q2367215; PIDN:AAC76395.1; PID:y2367216;
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
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Hypothetical 47.5 kD protein in cysG-LrpS intergenic region - Escherichia coli (strain hypothetical 47.5 kD protein in cysG-LrpS intergenic region - Escherichia coli (strain Syspecies: Escherichia coli (strain Syspecies: Escherichia coli (strain Syspecies: Escherichia coli (strain Syspecies: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 17-Mar-2000 (strain Shaco, F. R.: Plunkett III, G.: Bloch, C.A.: Perna, N.T.: Burland, V.: Riley, M.: G. A.: Rose, D.J.: Mau, B.: Shao, Y. Science 277, 1453-1462, 1997 A: Title: The complete genome sequence of Escherichia coli K-12.
A: Reference number: A64720; MuID: 97426617
A: Recession: ES511
A: Residues: preliminary: nucleic acid sequence not shown; translation not shown A: Residues: 1-462 < BLAT.
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A:Residues: 1-239 «KAM»
A:Cross-references: DDBJ:AP000060; NID:95104188; PIDN:BAA79744.1; PID:95104429
                                                                                                Gaps
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Pred. No. 1.3e+02;
1; Mismatches 1;
Score 31; DB 2;
Pred. No. 1.8e+02;
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Score 30; DB 2; Pred. No. 70; 1; Mismatches

85.78; 66.78;

Query Match 85.7 Bost Local Similarity 66.7 Matches 4; Conservative

111 |: 105 FKPSWQ 110

3

1 FKPXWR 6

A; Experimental source: strain Kl C; Genetics:

85.78; 66.78;

Query Match 85.7 Bost Local Similarity 66.7 Matches 4; Conservative

:11 11 398 YKPLWR 403

RESULT

1 FKPXWR 6

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A;Gene: yhfM C;Superfamily: arylnine permease

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genome polyprotein - Newcastle disease virus (strain Beaudette C)
H.Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C.Species: Newcastle disease virus
C.Species: Newcastle disease virus
C.Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C.Accession: A26747
R.Yusoff, K.; Millar, N.S.; Chambers, P.; Emmerson, P.T.
Nucleic Acids Res. 15, 3961-3976, 1987
A.Title: Nucleotide sequence analysis of the L genc of Newcastle disease virus: homology
A.Reference number: A93665; MUID:87230982
                                                                                                                                                A;Residues: 1-962 <VON>
C;Comment: This protein monitors the extracellular signal such as nutrition and trans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Species: Streptomyces coelicolor
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #Lext_change 03-Dec-1999
C.Dates: 03-Dec-1999 #sequence_revision 03-Dec-1999 #Lext_change 03-Dec-1999
E.Seequer, K.: Harris, D.; James, K.D.; Parkhill, J.: Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
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A. Cross-references: EMBL:AL096837; PIDN:CAB48897.1; GSPDH:GN00070; SCUEDH:SCF47A.10c
A. Experimental source: Strain A3(2)
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A:Molecule type: mRNA
A:Residues: 1-2204 «YUS>
A;Cross-references: GB:X05399; NID:g60937; PIDN:CAA28985.1; PID:g60939
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66.7%; Pred. No. 5.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%; Score 30; DB 2; Length 962; 66.7%; Pred. No. 2.6e+02; Live 1; Mismatches 1; Indels
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C;Reywords: ATP; nucleotidyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                   F.180-198/Domain: transmembrane *status predicted <TW4> F.255-273/Domain: transmembrane *status predicted <TW5> F.622-640/Domain: Lransmembrane *status predicted <TW6> F.621-679/Domain: transmembrane *status predicted <TW6> F.661-779/Domain: transmembrane *status predicted <TW6> F.661-779/Domain: transmembrane *status predicted <TW6> F.661-779/Domain: transmembrane *status predicted <TW6> F.661-779/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/F.679/
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F:56-74/Domain: transmembrane #status predicted <TMl>
F:91-109/Jourain: transmembrane #status predicted <TM3>
F:139-157/Domain: transmembrane #status predicted <TM3>
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A:Accession: T3643
A:Stalus: preliminary: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
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                          A;Accession: JC5808
A:Status: nucleic acid sequence not shown
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Matches 4; Conservative
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Matches 4; Conserv
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                                                                                                        A: Molecule type: DNA
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| 56 FKPNWK 161
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                                                                                                                                                                                                                                                                                                         A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Molecule type: DNA
A:Wesidues: 1-684 <WILL>
A:Residues: 1-684 <WILL>
A:Cross-references: EMBL:AL117195; NID:e1549729; PIDN:CAH55023.1; CESP:Y57A10A.r
A:Experimental source: clone Y57A10A
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N:Alternate names: hypothetical protein D2749
C:Species: Saccharomyces cerevisiae
C:Species: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 29-Oct-1999
C:Species: Caenorhabditis elegans
C:Date: 29-Oct.1999 #sequence_revision 29-uct.1999 #lext_change 29-Oct.1999
C:Accession: T31640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Genetics: ::
A:Gene: CESP:(57Ai0A.r
A:Introns: 108/3: 132/3: 149/1: 180/3: 323/2: 430/1: 530/1: 584/2: 647/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Accession: JC5808
R:Yun, C.W.: Tamaki, H.: Nakayama, R.: Yamamoto, K.: Kumagai, H.
Hiochem. Biophys. Res. Commun. 240, 287-292, 1997
A;Tille: G-prolein coupled receptor from yeast Saccharomyces cerevisiae.
A:Relerence number: JC5808; MUID:98049822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·.
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G protein-compled receptor 1 - yeast (Succharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Species: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 30; DB 2; Length 684
Pred, No. 1.9e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F:140-156/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;57-73/Domain: transmembrane #status predicted <TMI>F;92-108/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Paulin, L.; Saren, A.M.; Laamanen, P.
submitted to the Protein Sequence Database, July 1996
A.Reference number: 867560
A;Accession: 867568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 2;
Pred. No. 2.6e+02;
                                                                                                                                                                              submitted to the EMBH. Data Library, September 1999 A:Reference number: 221048 A:Accession: T31640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A: Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 66.7
Matches 4: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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A; Residues: 1-961 <PAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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672 FKPKWK 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: MIPS: YDL035c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 1:
FKPNWK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C: Accession: S67568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 PKPXWR 6
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RESULT

156

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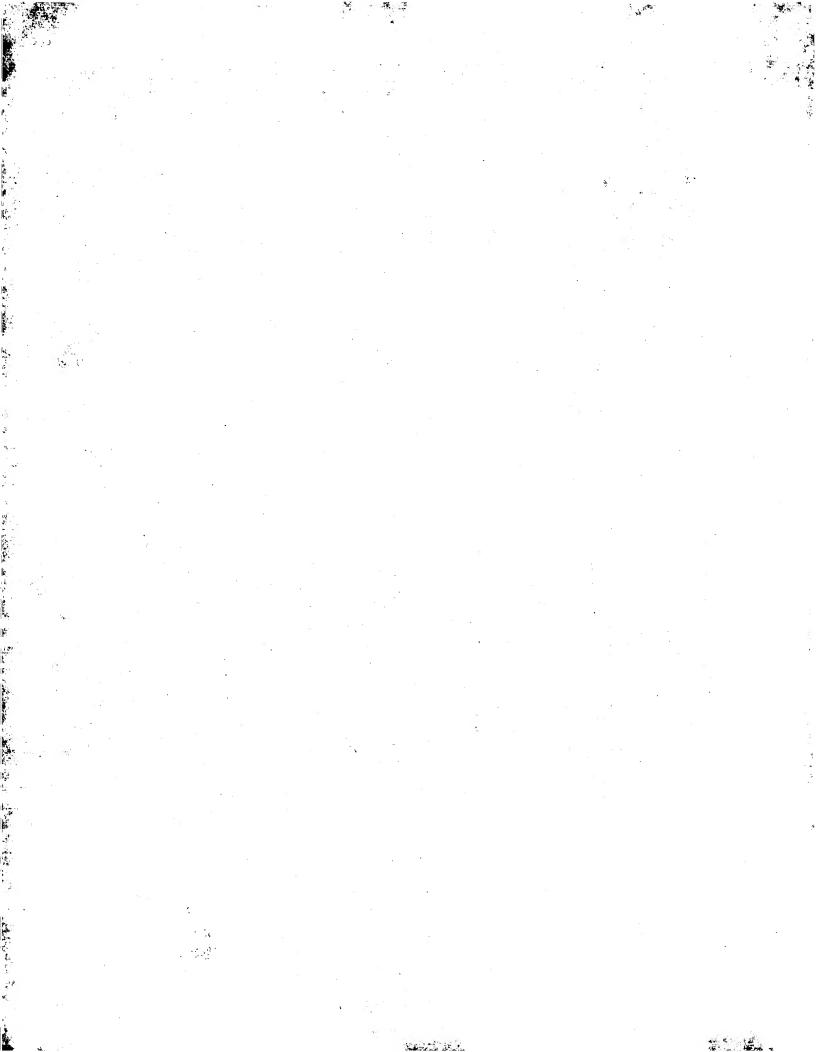
Matches

0; Gaps Oucry Match 82.9%; Score 29; UB 2; Length 119; Best Local Similarity 66.7%; Pred. No. 57; Matches 4; Conservative 1; Mismatches 1; Indels

0;

1. FKPXWR 6 1:1 || 36 FEPGWR 41 g ò

Search completed: February 27, 2002, 11:45:19 Job time: 698;3ec



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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 27, 2002, 11:42:45; search time 78.39 Seconds (without alignments) 2.806 Million cell updates/sec

US-09-446-109A-8 35 1 FKPXWR 6 Title: Periect score:

Sequence:

HI.OSUM62 Scoring table:

Gapup 10.0 , Gapext 0.5

100059 seqs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwlssProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CHMMADID

		d			SUMMARIES		
Result		Query					
SC.	Score	Match	Length	an i	61	Description	t i.on
-	33	94.3	535		YHILECOLI		escherichia
7	33	94.3	623	-	PTR2_CANAL		candida alb
'n	31	88.6	807	-	YM91_SCHPO		schizosacch
4	30	85.7	445	-	YHFM_ECOLI	_	escherichia
S	30	85.7	2204	_	KKPINDVB	_	newcastle d
9	29	82.9	217	-	YEDK_ECOL!	_	escherichia
7	56		452	-	SPS2_MOUSE	_	mus musculu
ස	29		477	-	Y264_SYNY3		synechocyst
c	58	82.9	-	-	GSH1_BRAJU		brassica ju
10	29	82.9	522	٦.	GSH1_ARATH		arabidopsis
Ξ	29		554	-	HS'TM_MOUSE		mus musculu
13	28	80.0	151	-	HSPD_BRAJA		bradyrhizob
13	. 58	80.0	151	_	HSPH_BRAJA		bradyrhizob
14	28	80.0	162	-	YLF6_CAEEL		caenorhabdi
15	28	80.0	167	-	CGC6_HUMAN		homo sapien
16	28	80.0	204	-	DSBA_LEGPN		legionella
17	28	90.0	233	-	VENV_BEV		berne virus
9	28	80.0	300	-	CYPE_DROME		drosophila
16	28	80.0	337	-	YHJD_ECOL.I		escherichia
. 20	. 28		340	-	C5AR_GORGO		gorilla gor
21	28	80.0	340	-	C5AR_PANTR	_	pan troglod
22	28	80.0	347	-	CSAR_MOUSE		mus muscalu
53	28	80.0		-	C5AR_HUMAN	_	homo sapien
24	28	80.0		_	C5AK_KAT	P97520 1	rattus norv
25	28	80.0	388	_	DXK_BACSU		bacillus su
56	28	•	405	-	HS47_CHICK	_	gallus gall
27	28	80.0	417	-	HS47_HUMAN	6	homo sapien
28	28	80.0	417	_	HS47_MOUSE	_	mus muscala
29	28	80.0	417	-	HS47_KAT		rattus norv
30	28	80.0	418	_	CRP2_HUMAN	_	homo sapien
≅ :	. 2H	80.0	469	-	RDXA_KHOSH		rhodobacter
35	58	80.0	482		C3AR_HUMAN	016581	homo sapien
E E	28	80.0	482	-	PUR8_YEAST		saccharomyc

90 1 C883_ARATH 601 1 YDF7_SCHPO 108 1 GLPK_WYCLF 139 1 V70K_PLRV1 143 1 POL_MIVAK 101 1 PODK_TREPA 101 1 PODK_TREPA 101 1 Y5GO_CLOAB 182 1 HBL1_CAEEL 133 1 ATY9_TEWTH 134 1 POL_MIVAY 175 1 RFBC_MIVAY	10.0 490 1 C883_ARATH 10.0 501 1 YDFSCHPO 10.0 508 1 GLPK_MYCLF 10.0 639 1 VOK_PLRV1 10.0 843 1 POL_MIVAK 10.0 901 1 PODK_TREPA 10.0 967 1 Y5GCLOAB 10.0 962 1 HBLL_CAEEL 10.0 1133 1 ATX9_TETTH 10.0 1135 1 RFBC_MIVAX	023051 arabidopsis	Q10479 schizosacch	Q9cb81 mycobacteri	P17519 potato leaf	P03357 akr murine	O83728 treponema p	P55465 rhizoblum s	P33747 clostridium	09xyd3 caenorhabdi		P03356 akv murine		
000 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		C883_ARATH	YDF7_SCHPO	GLPK_MYC1.F	V70K_PLRV1	POL_MLVAK	PODK_TREPA	Y4GI_RHISN	YSGO_CLOAB	HBL1_CAEEL	ATX9_TETTH	POL_MLVAV	RFBC_MYXXA	
		90 1	01 1	08 1	39 1	43 1	01 1	09 1	67 1	82 1	33 1	96 1	75 1	
		34	3.5	33	3.7	36	 	4.0	-	~1	4.3	44	10 15	,

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STACKNENTZ / MG1655; MG1650; MG1618 D.L., Plunkett G. 111, Blattuer F.R.; MG14ysis of the Escherichia coli genome. V. DNA sequence of the Escherichia coli genome. V. DNA sequence of the caption from 76.0 to 81.5 minutes: "; MG161 MG16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=KI2 / MG1655;
MSDLINE=97426617; PubMed=9278503;
STALINE=97426617; PubMedE G. III, Bloch G.A., Perna N.T., Burland V., St.Leg F.R., Plunkett G. III, Bloch G.A., Perna N.T., Burland V., St.Leg M., Collado-Vides J., Glasner J.D., Rode G.K., Mayhew G.F., Stegor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Wu B., Shap Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enteria; Proteobacteria; gamma subdivision; Enterobacterlaceae;
Escherichia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jupusblished observations (JUN-1999).
-:- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS INTRODUCED IN POSITION 399 TO PRODUCE THIS ORF.
                                                                                                YILL_ECOLI STANDARD: PRT; 535 AA.
P37629; P37628;
01-0CT-1994 (Rcl. 30, Creatcd)
20-AGG-2001 (Rcl. 40, Last sequence update)
120-AGG-2001 (Rcl. 40, Last sequence update)
120-AGG-2001 (Rcl. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The complete genome sequence of Escherichia coli K-12."; Selence 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4/porthetical protein: Complete proteome.
5-20 ENCE 535 AA; 61576 MW; 0046CE539989FDF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ### AE000425; AAC76514.1; ALT_FRAME. ##BL: AE000425; AAC76515.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :43'; U00039: AAB18465.1; AUT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U00039; AAB18466.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EG12227; yhit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Semerichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEST_TaxID+552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KICH K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E. M. Jene;
                                                  XIIILES: ALI
RESITES
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11tch . One

94.3%; Score 33; DB 1; Length 535;

Matches

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PTR2_CANAL

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                                                                                                                                                                                                                      Laug B.F., Ahue F., Bonen L.;
The mitochondrial genome of the fission yeast Schizosaccharomyces pombe. The cylochrome b gene has an intron closely related to the first two introns in the Saccharomyces cerevisiae cox1 gene.";
J. Mol. Biol. 184:333-366(1985).
                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YHEM_ECOLI STANDARD; PRT; 445 AA.
24539; P76686;
01-NOV-1995 (Rel. 32, Created)
20-AUG-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 47.5 KDA PROTEEN IN CYSG-TRPS INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.6%; Score 31; DB 1; Length 807; 66.7%; Pred. No. 78;
tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Mitochondrion.
SEQUENCE 807 AA; 91637 MW; AFD70F35£84CAA8F CRC64;
                                                                                                                     Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                       Schizosaccharomycetales; Schizosaccharomycetaceae;
                01-NOV-1988 (Rel. 09, Created)
15-DKC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PACCHEFICAL, 91 KDA PROTEIN IN COB INTRON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - SIMILARITY: TO GROUP II INTRON MATURASES
                                                                                   Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interPro; IPR000442; Intron_maturse2_InterPro; IPR000477; RVTse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01348; Intron_maturas2; 1.
Efam; PF00078; rvt; 1.
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                                                                                                                                                           Schizosaccharomyces.
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Matches 4; Conserv
                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                         NCHI_TaxID=4896
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                                                                                                     Milochondrion.
                                                                                                                                                                                                                                                                                                                                                                              STRAIN-AD7-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FKPXWR
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                   Gaps
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Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBL_TaxID=5476;
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                   Indels
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                 <u>:</u>
                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDE TRANSPORTER PTR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane.
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Pred. No. 25;
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Pred. No. 22;
0; Mismatches
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                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CBS 562 / ATCC 18804;
MEDLINE-95291458; PubMed-7773409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pram; PF00854; PTR2; 1.
PROSITE; PS01022; PTR2_1; 1.
PROSITE; PS01023; PTR2_2; 1.
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83.3%;
 83.3%;
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                   Conserval ive
                                                                                                                                                                         STANDARD;
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Hest Local Similarity
Matches 5; Conserv
 Best Local Similarity
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445 FKPIWR 450
                                                                                   168 FKPDWR 173
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                                                   1 FKPXWR 6
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ID YM91_SCHPO
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P46030;
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SEQUENCE FROM N.A.

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PIR; A26747; RRNZNV.
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Best Local Similarity
Matones 4: Conserv
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15-DEC-1998 (Rel. 37, Last annotation update)
RNA POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LARGE STRUCTURAL PROTEIN)
        MEDLINE-97426617; PubMed-9278503; Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                     SUBCELLULAR LOCATION: INTECRAL MEMBRANE PROTEIN, INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIANG-87230982; PubMed-3035486;
Yusoff K., Millar N.S., Chambers P., Emmerson P.T.;
"NucleoLide sequence analysis of the L gene of Newcastle disease
virus: homologies with Sendai and vesicular stomalitis viruses.";
                                                                                                                                                                                                                                                                                       Pfam: PF00324; aa_permeases; 1.
Hypothetical protein; Transport; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                           SIMILIARITY: BELONGS TO THE ARCH/CAUB/GERAB/LYSI FAMILY OF
                                                  Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Newcastle disease virus (strain Heaudette C/45) (NDV).
Viruses; ssRNA negative-strand viruses; Mononeyavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        B98DF5944A5E1FEF CRC64;
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Pred. No. 71;
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InterPro; IPR002293; AA_rel_permease_1.
InterPro; IPR002027; Amino_acid_permease.
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EMBL; AEU00413; AAC76395.1; ALT_INIT.
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01-JUL-1989 (Rel. 11, Last seq
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Rest Local Similarity
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                                                                                                ( POTENTIAL.).
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155
181
236
273
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381 YKPLWR 386
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P11205;
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Nucleic Acids Res. 15:3961-3976(1987).

-: FOUCTION: PROBABLE COMPONENT OF THE ACTIVE FOLYMERASE. IT MAY FUNCTION IN MENA SYNTHESIS, CAPPING, METHYLATION AND POLY(A) SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MENAS, RNA EDITING OF THE PURPLE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.

-: SIMILARITY: WITH I PROTEIN OF OTHER PARAMYXOVIRUSES.
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MEDLINE=97426017; PubMed=9278503;
HISTEDE FIR., Plunkett G. III, Bloch C.A., Perna N.T., Hurland V.,
RISTHEF V. Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Glegor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rada M., Kihara M., Kawaqishi I., Macnab R.M.; "Opgunization of the Escherichia coli and Salmonella typhimurium thromosomes between flaggilar regions Ilia and Ilib, including a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-NOV-1997 (Rel. 35, Last sequence update)
2.1-AUG-2001 (Rel. 40, Last annotation update)
37-POTHETICAL 24.5 KDA PROTEIN IN AMYA-FLIE INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 30; DB 1; Length 2204;
Pred. No. 3e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerase.
v; C67B8674D904802C:СкС64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001016; Paramyx_RNA_pol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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Transferase; RNA-directed RNA po
SEQUENCE 2204 AA; 248822 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X05399; CAA28985.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 85.7%;
Similarity 66.7%;
4: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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YZ64_SYNY3
P73436;
 ACT_SITE
SE_CYS
SITE
                                                      NP_BIND
DOMAIN
DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                 SLL1464
                                                                                                                                                                                                                                                                                YZ64_SYNY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -: FUNCTION: SYNTHESIZES SELENDHOSPHATE FROM SELENIDE AND ATP.
                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
85-ERLENIDE, WATER DIKINASE 2 (EC 2.7.9.3) (SELENDEHATE SYNTHETASE 2)
(SELENIUM NONOR PROTEIN 2)
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of a novel selD homolog from eukaryotes, bacteria, and archaea: is there an autoregulatory mechanism in selenocysteine metabolism?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

BEDLINE-97140286; Pubmcd-8986768; Current A., Cocks B.G., Copeland N.G., Culmaracs M.J., Peterson D., Vicari A., Cocks B.G., Copeland N.G., Cilbert D.J., Jenkins N.A., Perrick D.A., Kastelein R., Bazan J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- COPACTOR: SELENOCYSTEINE. THE ACTIVE-SITE SELENOCYSTEINE IS ENCODED BY THE OPAL COLON, UGA.
-1- SIMILARITY: HELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-96017645; PubMed-7588067;
MEDLINE-96017645; PubMed-7588067;
MILES M.J., Bazan J.F., Zlotnik A., Wiles M.V., Grimaldi J.C.,
foce F., McClanahan T.;
*A new approach to the study of haematopoictic development in the
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Melazoa; Chordata; Craniata; Vertehrata; Euteleostomi;
Mammalia; Futheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                   ö
                                                             Hypothetical protein: Complete proteome.
Hypothetical protein: Complete proteome.
CONFLICT 213 217 TRRS -> NGGAELIUPV (IN REF. 1).
SEQUENCE 217 AA: 24500 MW: 4F26C95DB3B02900 CRC64;
                                                                                                                                                    82.9%; Score 29; DB 1; Length 217; 66.7%; Pred. No. 57;
Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 93:15086-15091(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase: Selenium; Selenocysteine; ATP-binding.
                                                                                                                                                                                                                                                                                                           152 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
             EMBL: L13279; -; NOT_ANNOTATED_CDS
EMBL; AE0U0285; AAC74998.1; -.
                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:108388; Sps2.
InterPro; 1PK000728; AIRS_related.
Piam; PF00586; AIRS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yolk sac and embryoid bodies.";
Development 121:3335-3346(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U43285; AAC53024.1; -.
                                         RcoGene; EG13278; yedk.
InterPro; IPR003738; DUF159.
                                                                                                                                                    Query Match... 82.9
Best Local Similarity 66.7
Matches 47. Conservative
                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASS I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_Tax10-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHATE
                                                                                                                                                                                                                                      87 FKPLWO 92
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                                                                                                                                                                                                                                                                                                        SPS2_MOUSE
P97364;
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                                                                                                                                                                                                                                                                        Gaps
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Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Mijajima N., Hirosawa M., Sujuira M., Sasamoto S., Kimura T.,
Hisouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
Okumura S., Shimpo S., Takeuchi C., Wada T., Walanabe A.,
Yamada M., Yasuda M., Tabatas S.;
Saguence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
GHILLE genome and assignment of potential protein-coding regions.";
DNA Res. 3.109-136(1996).
                                             IMPORTANIT FÜR CAITALYTLIC ACITIVITY (BY
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                                                                                                                                                                                                                           Length 452;
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Pred. No. 1.1e+02;
0; Mismatches 2; Indels
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SEQUENCE 477 AA: 54041 MW; 81F6899B1A6D613C CRC64;
                                                                                                                                                        9DA6F7250CFE80E4 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-JUL-2001 (Rel. 40, Last annotation update)
HYPOTHEFICAL 54.0 KDA PROTEIN SLL1464.
                                                                                     ATP (POTENTIAL).
POLY-ALA.
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                                                                     SIMILARITY)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (strain PCC 6803)
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                                                                                                                                                        47786 MW;
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Pfam; PF02696; UPF0061; 1.
                                                                                                                                                                                                                        82.98;
66.78;
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                                                                                                                                                                                                   Oucry Match
Best Local Similarity 66.77
Best A; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1148;
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433
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ID GSH1_BRAJU
AC 023736; Q43389;
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63
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48 FSPSWR 53
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us-09-446-109a-8.rsp

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GLUTAMATE--CYSTEINE LIGASE, CHLOROPLAST PRECORSOR (EC 6.3.2.2) (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS).
GSH1 OR AT4G23100 OK F7H19.290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                            JEQUENCE FROM N.A
                                                                                                                                                                                                                  WCB1_TaxID-3702;
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
GLUTAMATE--CYSTEINE LIGASE, CHLUNOPLAST PRECURSOR (RC 6.3.2.2) (GAMMA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUNCELLUIAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-!- MISCELLANBOUS: IN PLANTS, THERE ARE TWO FORMS OF THIS ENZYME, ONE CYTOSOLIC AND THE OTHER CHLOROPLASTIC.
                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE-99281577; PubMcd-9620267; Schaefer H.J., Haag-Kerwer A., Rausch T.; schaefer H.J., Haag-Kerwer A., Rausch T.; colby of the heavy-metal accumulator Brassica juncea L.: evidence in roots of the heavy-metal accumulator Brassica juncea L.: evidence for Cd-induction of a putalive milochondrial gamma-glutamylcysteine synthetase isoform.";
                                                                                                                                                                                                      Eukaryota; VIridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - PATHWAY: FIRST AND RATE-LIMITING STEP IN DE NOVO GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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TRANSIT 1 55 CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.9%; Score 29; DB }; Length 514; 66.7%; Pred. No. 1.3e+02;
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GLUTAMATE--CYSTEINE LIGASE.
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07C71CB13E785FA8 CRC64;
                                                                                                                                                                                 Brassica Juncea (Leaf mustard) (Indian mustard).
                                                                                                                    GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS)
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T -> I (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Mol. Biol. 37:87-97(1998).
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                                                                                                                                                                                                                                                                                                  NCB1_Tax ID=3707;
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CONFLICT CONFLICT SEQUENCE CONFIL COT

Query Match

Matches

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GSH1_ARATH 1D GSH1_A AC P46309 DT 20-AUG DT 20-AUG

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MEDINE-2008 NAS.

REATINE-CONGNARABI
REATINE-CONGNA
                                                                                  Bakaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosidae;
enrosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The glutach considering adminm-sensitive mutant, cad2-1, of Arabidopsis challene is deficient in gamma-glutamylcysteine
                                                                                                                                                                                                                                                                                                                            structurally unrelated to mammalian, yeast, and Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. LANDSBERG ERECTA;

Julimann P., Gondet L., Bach T.J.;

"Isolation of an Aribidopsis thaliana cuna encoding a putative damma-glutamylcysteine synthetase by complementation of a GSHI delicient yeast mutant-glutamylcysteine synthetase.";

Submitted (JSC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                             STRAIN-CV COLUMBIA; TISSUE-Leaf;
MDDLINE-29023984; Pubmed-7937837;
MAY M.J., Leaver C.J., Leaver C.J.,
"Arabidopsis thaliana gamma-glutamylcysteine synthelase is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 91:10059-10063(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cobbett C.S., May M.J., Howden R., Rolls B.
                                                                 Arabidopsis thaliana (Mouse-ear cress).
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MEDLINE-93326638; PubMed-7916639;
                                                                                      carboxylesterase in mouse liver.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; S64130; AAB27606.1; -.
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554 AA:
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Best Local Similarity
Matches 4; Conserv
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND DESCRIPTION OF THE REPORT 
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GLUTAMATE--CYSTEINE LIGASE.
A -> T (IN STRAIN LANDSBERG ERECTA).
Y -> N (IN STRAIN LANDSBERG ERECTA).
VRTGVTPAEKLLEMYNGEWGOSVDPYFEELLY -> GONRS
YACGEALGDVQWRMGTKRRSRVRRAAVLRKWDVNKRCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
11-NOV-1997 (Rel. 35, Last annotation update)
11-NER CARHOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ES-MALE) (ESTERASE-31).
                                                                                                                                                                                                                                                                                                                                                                                               -:- SÜRÜNIT: MONOMER (PROHAHLE).
-:- SÜHCELLULAR LÖCATION: CHIÖROPIAST (PROBAHLE).
-:- TISSUE SPECIFICITY: ABUNDMYT IN LEAVES AND ROOTS.
-:- MISCELLANBOUS: IN PLANTE, THERE ARE TWO FORMS OF THIS ENZYME, ONE CYTOSOLIC AND THE OTHER CHLOROPLASTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Nelson J., Spielh J., Ryan E., Andrews S., Geisel C., Layman D., Du H., Ali J., Berghoff A., Jones K., Droue K., Cotton M., Joshu C., Antonolu B., Zidanic M., Strong C., Sun H., Lemmar H., Yordan C., Shalong J., Preston K., Vil D., Shekhor M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy W., Haseagaw A., Hammed A., Lodhi M., Johnson A., Chen E., Marra M., Martlenssen R., McComble W. R., Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + L-CYSTEINE - ADP + ORTHOPHOSHATE + GAMMA-L-GLYAMYLL-CYSTEINE.

-i- ENYME REGULATION: FEEDBACK INHIBITION BY GLUTATHONE.

-i- PATHWAY: FIRST AND RATE-LIMITING STEP IN DE NOVO GLUTATHIONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast; Transit peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.9%; Score 29; DB 1; 1
66.7%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 AA.
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STRAIN-BALB/GJ X DBA/2J; TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y09944; CAA71075.1; -.
                                                                                                                                                                                                                                        Nature 402:769-777(1999).
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                               BIOSYNTHESIS
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Q63880;
                                                                                                                                                                                                                    thallana.
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RESULT 11 FS.FM_MOUSE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RETICULUM.
-!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ.
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                                                                                                                                                   THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
--- CAPALATIC ACTIVITY: A CARBOXYLIC ESTER + H(2)O - AN ALCOHOL
--- SUBCELLUGAR LOCATION: MICROSOMAL MEMBRANE, LUMEN OF ENINOPLASMIC
                                                                                        Biochim, Biophys, Acta 1174:72-74(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Narberhaus F., Weiglhofer W., Fischer H.M., Hennecke H.;

Narbertfication of the Bradyrhizobium japonicum deup gene as part, an operon containing small heat shock protein genes.";

Submitted (NOV-1997) to the EmbLyGenBank/DDBJ databases.

:- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00122; CARBOXYLESTERASE B_1; 1.
PRUSITE; PS00941; CARBOXYLESTERASE B_2; 1.
Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reliculum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
Aida K., Moore R., Negishi M.; "Closing and nucleotide sequence of a novel, male-predominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 554;
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80.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 1;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI 102773; Es31.
InterPro: IPR002018; Carboxylesterase_B.
InterPro: IPR000379; Est_lip_thloest_actsite.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94150718; PubMed-7906398; Baynes C., Berks M., Milson R., Alnacough R., Anderson K., Baynes C., Berks M., Hilson R., Alactough R., Anderson R., Eavello A., Fraser A., Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A., Creen P., Hawkins T., Hilliot L., Jier M., Johnston L., Johnston L., Johnston L., Johnston L., Johnston L., Johnston L., Santaner B., O'Callaghan M., Latrellle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Latrellle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shownkeen R., Sims M., Smaldon N., Smith A., Smith A., Swith A., Swith M., Sounders D., Studen R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Materson R., Watson A., Weinstock L., Wilkinson-Sproat J., R.
                                                                                                                                                                                                                                                                                                                                                                                                                                Enkaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                       91.FEB-1994 (Rel. 28, Created)
51.FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 18.5 KDA PROTEIN C40H1.6 IN CHROMOSOME ILL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ul protein.
162 AA; 18537 MW; BDC03CE3BCE79D55 CRC64;
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39-MAY-2009 (Rcl. 39, Last sequence update)
22-ANG-2001 (Rel. 40, Last annotation update)
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Pred. No. 68;
0; Mismatches
                                                                                                       PRT;
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80.0%;
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                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              themo sapiens (Human)
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                                                                                              YUF6_CAERL
Q04598;
Q1:FEB-1994 (
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This SWISS-PROT cntry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are to restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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"Occurrence of a superfamily of small heat shock proteins in
Bradyrhizobium japonicum and other Rhizobium species: a plant-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
NCBL_Tax(D-375;
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Submitted (AUG-1998) to the EMHI,/GenBank/DDHJ databases.
-!- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
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SEQUENCE 151 AA; 17098 MW; DFE9809310AF6A28 CRC64;
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66.7%; Pred. No. 64;
ive 0; Mismatches 2
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Pred. No. 64;
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InleFPro; IPR002068; Crystallin_HSP20.
Priam: PE000L; HSP20: 1.
PROSITE: P601031; HSP20: 1.
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Ptam; PF00011; HSP20; 1.
PROSITE; PS01031; HSP20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heat shock; Multigene family.
SEQUENCE 151 AA; 17272 MW;
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66.7%;
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6 FSPLWR 11
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6 FSPLWR 11
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167 AA.

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Thu Feb 28 11:23:41 2002
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                      Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
"Identification of novel human genes evolutionarily conserved in
Caenorhabditis elegans by comparative proteomics.";
Genome Res. 10:703-713(2000).
-i- SIMILARITY: STRONG, TO C.ELEGANS C40H1.6.
MEDLINE-20272150; PubMed-10810093;
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ö Gaps ö Ouery Match 80.0%; Score 28; DB 1; Length 167; Best Local Similarity 80.0%; Pred. No. 70; Matches 4; Conservative 0; Mismatches 1; Indels

EMBL; AF151884; AAD34121.1; · Hypothetical protein. SEQUENCE 167 AA: 19458 MW; 1675D9187DC43E14 CRC64;

1 FKPXW 5

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121 FKPLW 125 ã

Search completed: February 27, 2002, 11:42:45 Job time: 544 sec

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Gentore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 27, 2002, 11:50:09 : Search time 281.76 Seconds (without alignments) 3.115 Million cell updates/sec Run on:

US-09-446-109A-8 :35 1 FKPXWR 6 Title: Perfect scorer: Sequence:

HLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 seqs, 146272329 residues Searched:

473505 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL_17:* Database :

sp_archea:* sp_bacteria:* sp_fungi:* sp_human:*

sp_virus:* sp_vertebrate:* sp_unclassified:* sp_invertebrate:* sp_mhc:* sp_organelle:* sp_rodent:* sp_plant:. sp_mammal:* sp_phage: •

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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NO.	Score	Match	Match Length DB	80	10	Description
-	34	97.1	250	. ~	Q9EUM2	O9eum2 corvnebacte
2	88	94.3	380	-	057935	
3	33	94.3	498	7	083784	083784 treponema p
₹	33	94.3	623	٣	Q9URI.7	Ogurl7 candida alb
S	33	94.3	917	ŗ.	94XXPQ	O9xyp8 drosophila
9	33	94.3	917	ស	Q9VY94	09vv94 drosophila
7	31	88.6	221	10	Q9X.112	O9xi12 orvza sativ
8	30	85.7	204	Ξ	Q9D3F2	O9d3f2 mus musculu
6	30	85.7	239	_	09YE03	O9ye03 aeropyrum p
10	30	85.7	440	Ξ	0913981	Ogd9rl mus musculu
=	30	85.7	909	~	031566	031566 bacillus su
12	30	85.7	610	~	052961	052961 bacillus su
13	30	85.7	684	'n	Q9NA80	Q9na80 caenorhabdi
14	30	85.7	961	~	012361	Q12361 saccharomyc
15	30	85.7	1232	2	100,160	0911q1 arabidopsis
16	30	85.7	2204	12	090341	090341 newcastle d
17	30	85.7	2204	12	9HWM60	Q9wmh6 newcastle d
18	30	85.7	2204	12	. O9DLD3	Q9dld3 newcastle d
19	30	85.7	2454	~	Q9UVP2	Q9uvp2 emericella

		O9cjpU pasteurella O9njyl glardia lam	O9n2y6 caenorhabdi O9f2r9 streptomyce	09fs78 triticum ac	_		O26470 methanobact	Q9a710 caulobacter	Ogrwe3 deinococcus	091m75 arabidopsis	Oscib2 gibberella		Q9c1b9 fusarium sp	Q9kn89 vibrio chol	Q40414 nicotiana s	Q52729 rhizobium e	Q9yq81 aeropyrum p		042902 schizosacch
3 Q9UV56 2 Q9XAA5	2 Q92EW4 5 O96402	2 09CJP0 5 09NJY1	2 Q9F2R9	10 Q9FS78	2 033353	5 Q22568	1 026470	2 09A710	2 Q9RWE3	10 Q9LM75	3 09C1B2	3 094088	3 Q9C1B9	2 Q9KN89	10 040414	2 Q52729	1 Q9YG81	2 Q9HTC7	3 042902
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Tauch A., Puehler A., Kalinowski J.;
I'mA Sequence and genetic Organization of the integron-carrying R-plasmid pCG4 of Corynobacterium glutamicum.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL3 FR164956, AG600294.1;
TherPro: IPR002145; CopG_HTH_4.
                                                                                                                Corynobacterium glutamicum (Brevibacterium flavum).
Plasmid R-plasmid pCG4.
Backeria, Firmicutes: Actinobacteria; Actinobacteridae;
Actinomyceriales: Corynebacterineae; Corynebacteriaceae;
Corynebacterium.
                                                                                                                                                                                                                                                                                                                                           SHOULDINGE 250 AA; 28804 MW; 1950863678483157 CRC64;
                                                 Created)
Last sequence update)
Last annotation update)
                        250 AA.
                          PRT;
                                                 (TrEMBLrel. 16, TrEMBLrel. 16, (TrEMBLrel. 17,
                          PRELIMINARY;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
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01-MAR-2001 (
01-JUN-2001 (
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                                     QUEUM2
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Caps ö 97.1%; Score 34; DB 2; Length 250; 83.3%; Pred. No. 35; 1; Indels 0; Mismatches Bes. Godal Similarity 83.3 Matches 5; Conservative Que:" Match

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EKPXWR 5 G G Š

380 AA.

us-09-446-109a-8.rspt

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Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Pujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.3%;
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83.3%;
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Pfam; PF02388; FemAB; 1.
                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 83.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
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                                                                           Venter J.C.;
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-:- COPACTOR: NICKEL (BY STHILANITY).
-:- PATHWAY: HYDROGEN METABOLISM; FHL PATHWAY (BY SIMILARITY).
-:- SUBUNIT: FHL COMPRISES OF A PORMATE DEHYDRAGENASE, UNIDENTIFIED
ELECTRON CARRIERS AND A HYDROGENASE (ISOGNIZME 3). IN THIS NON-
ENERGY CONSERVING PATHWAY MOLLECULAR HYDROGEN AND CARBODICAIDE FROM
FORMATE ARE RELEASED (HY SIMILARITY).
-:- SIMILARITY: HELONGS TO THE COMPLEX I 49 KDA SUBUNIT FAMILY.
--- EMBL: U67501; AAB98504.1;
01-JAN-1998 (TTEMBLICEL. 05, Created)
01-JAN-1998 (TTEMBLICEL. 05, Last sequence update)
01-JUN-2001 (TTEMBLICEL. 17, Last, annotation update)
PUTATIVE FORMATE HYDROGENLYASE SUBUNIT 5 (FHL SUBUNIT 5) (HYDROGENASE-
                                                                                                                                                                                                                                                                           PERIOR NO. 17, 70 DS 2661 / ATCC 43067;

MEDLIKE-96337999; PubMed-8688087;

MEDLIKE-96337999; PubMed-8688087;

Bull. C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sulton G.G., Blake J.A., Filzderald L.M., Clayton R.A., Gocayne J.D.,

Kerlavaqe A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Ovorbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.J., Googhagen N.S.M., Weidman J.F., Fuhrmann J.L., Nupyen D.,

Uttcrback T.R., Kolley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Collon M.D., Roberls K.M., Hurst M.A., Kaine B.P., Boordovsky M.,

Klenk H.-P., Fraser C.M., Smilth H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam: PF00346; complex1_498d; 1.
Pfam: PF00374; NiFeSc_Hases: 1.
PROSITE: PS00535; COMPLEX1_498; UNKNOWN_1.
PROSITE: PS00507; NI JIGENASE_L_1: UNKNOWN_1.
Hypothetical protein: Oxidoreductase: NAD; Iron-sullur: 4Fe-4S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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MEDLINE-98332770; Pubmed-9665876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 273:1058-1073(1996).
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SEQUENCE 380 AA: 43638
                                                                                                                                           Methanococcus jannaschii.
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Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treponema pallidum.
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                                                                                               COMPONENT E).
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083784
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"A Candida aibicans Genome Project: Cosmid Contigs, Physical Mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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"Complete genome sequence of Treponema pallidum, the syphilis spirochete.";
Science 281:375-388(1998).
EMBAL; ARC65773.1; -.
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                                                                                                                                                                                                                                                                              Length 498;
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Murphy L., Harris D.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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PUTATE PER PTR2; 1.
PRINT PP00854; PTR2, 1.
PROSTTE; PS01023; PTR2, 2; UNKNOWN_1.
PROSTTE; PS01023; PTR2, 2; UNKNOWN_1.
                                                                                                                                                                            Complete protecime.
SEQUENCE 498 AA, 56074 MW; 81710E41264431H8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence updatc)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
PEPTIDE TRANSPORT PROTEIN.
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                            Score 33; DB 2;
Pred. No. 1e+02;
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EMRI; AL033503; CAA22021.1; -.
InterPro; IPR000109; PTR2.
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Sasski T., Nagamura Y., Yamamoto K.;
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                                                                                                                                                                                                                                                                                                    EMBL; AE003493; AAF48309.1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Encal Similarity
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203 FRPTWR 208
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Q903F2;
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Adams M.D., Celoire PubMed-10731132;

Adams M.D., Celoire S.E., Holf. R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celoire S.E., Holf. R.A., Evans C.A., Gocayne J.D.,
A manatides P.G., Scherer S.E., Holf. W., Hoskins R.A., Galle R.E.,
A manatides P.G., Scherer S.E., Holf. W., Hoskins R.A., Galle R.E.,
A manatides P.G., Scherer S.E., Holf. W., Hoskins R.A., Galle R.E.,
A corge K.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A britch G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
A britch G.G., Bazter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A horll J.F., Aqbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A becson K.Y., Benos P.V., Berman B.P., Handari D., Bolshakov S.,
A borkova D., Hotchian M.R., Bouck J., Brokstein P., Brottier P.,
Butler K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A de Pablos B., Delcher A., Danlke C., Davenport L.B., Davis S.M.,
Budson K., Boup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA bodson K., Boup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A bolser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Classer K.,
A Fosler C., Gabriell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabriell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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L(1)DAO ON COLU988.
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda; Tracheata: Hexapoda; Insecta;
Pteryota: Moptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila.
                                                                                                                                                   Pteryyota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDILIKE-99156983; Vubked-10037793;
OGGENMA K., Wicse C., Nartin O., Milligan R.A., Iwamatsu A.,
Mitchisson F.J., Zhenq Y.;
"Characterization of two related Drosophila gamma-tubulin complexes that differ in their ability to nucleate microtubules.";
J. Cell Hiol. 144:721-733(1999).
EMHL, AF118380; AAD278171; --
FIYBASE; FBGN0001612; 1(1)dd4.
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                                                                                                   L(1)DD4 OR GGRP91 OR CG10988.
Drosophila metanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                          InterPro: IPR000634; dehydrtse_ser_thr.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
SEQUENCE 917 AA; 103819 MW; EBF2F41E35049D27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                          (TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 5; I
Pred. No. 1.9e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     917 AA.
                 917 AA
                                           01-NOV-1999 (TTEMBLICE) 12, Greated)
01-NOV-1999 (TTEMBLICE) 12, Last seq
01-IUN-2001 (TEMBLEE) 17, Last ann
GAMMA-TUBULIN RING PROTEIN DGRIP91.
                                                                                                                                                                                                                                                                                                                                                                                                                       94.3%;
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.35,
has 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELLIMINARY;
                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                             NCBI_TaxID-7227
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657 FKPLWR 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FKPXWR 6
             Q9XYP8
Q9XYP8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9VY94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09VY94
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RESULT
Q9VY94
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Addition D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C.,
Jaidli M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liak, Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
A. Liak, Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
A. Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
A. McExulov G. Milshina N.V., Mobarry C., Muzny D.M., Nelson D.L.,
A. McIshina N.V., McMary C., Muzny D.M., Nelson D.L.,
A. McIshina N.A., Nixon K., Nissern D.R., Pacleb J.M.,
A. Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A. Achinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
A. Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A. Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Mulliams S.M., Woodage T., Horley K.C., Mul D., Yang S., Yao Q.A.,
A. Mang X.-Y., West R.W., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.,
Xheng X.A., Myers E.W., Rubin G.M., Venter J.C.,
Xheng X.A., Wells E.W., Webland G.M., Venter J.C.,
Xheng X.A., Wells E.W., Wells G.M., Venter J.C.,
Xheng X.A., Wells E.W., Wells G.M., Venter J.C.,
Xheng X.A., Wells E.W., Wells G.M., Venter J.C.,
Xheng X.A., Myers E.W., Rubin G.M., Venter J.C.,
Xheng X.A., Myers E.W., Rubin G.M., Venter J.C.,
Xheng X.A., Wells A. W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.3%; Score 33; DB 5; Length 917; 83.3%; Pred. No. 1.9e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103706 MW; 6AEE88C211D256BB CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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66.7%; Pred. No. 1.2e+02;
tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 AA.
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erositE; PS00165; DEHYDRATASE_SER_THR; 1.
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EMUL: AP000060; BAA79744.1;
InterPro; IPR001454; Hydrolase.
InterPro; IPR000150; Hypothet_cof.
                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 4: Conservative
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                   1 FKPXWR 6
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                                                                                                                                                                                                                                   Query Match
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       SO EX DESCRIPTION SO EX DESCRI
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                                                                                                                                                                                                                                                                                                                      Arakawa T., Shinagawa A., Shibala K., Yoshino M., Itch M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Eukuda S.,
A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazawi Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadola K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
R. Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pescle G., Ouackenbush J.,
Schrim L.M., Staubli F., Sizuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Haldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carnhori P., de Bonaldo M.F.,
Gustincich S., Hill D., Hojunga N., Carnhori P., de Bonaldo M.F.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Mynshaw-Bootis A., Yoshida K., Haseqawa Y., Kawaji B., Kohtsuki S.,
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                                                                                                                                            Eukoryota: Melazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
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01-JUN-2001 (TrEMBLrel. 17, Crealed)
01-JUN-2001 (TrEMBLrel. 17, Last sequence updale)
01-JUN-2001 ("TEMBLrel. 17, Last annotation update)
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01-NOV-1999 (TrimHirel. 12, Last sequence update)
01-JUN-2001 (TreMELEE. 17, Last annotation update)
HYPOTHETICAL 24.8 KDA PROTEIN APE0766.
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                                                                                                                                                                                                                                                                       STRAIN-C57BL/6J; TISSUE-THYMUS;
MEDLINE-21089660; Pubmed-11217851;
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EMBL; AK017942; HAB31014.1; -.
MGD; MGI:1923275; 5830420C20Rik.
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Matches 4; Conservative
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                                                                         5830420C20RIK PROTEIN.
                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                     5830420C20R1K
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                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Marmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, Last sequence updale)
1-JUN-2001 (TrEMBLrel. 17, Last annotation updale)
ADULT MALE TESTS CDM. RIKEN FULL-LENGTH ENRICHED LIBRARY, CLONE: 1700030N20, FULL INSERT SEQUENCE.
                                                                                                                                                                                                                     Score 30; DB 1; Length 239;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                     1; Indels
Pfam; PF00702; Hydrolase; 1. PR087FF; PS01229; ODK. 27; UNNOW_1. Hyp: PS01229; ODE 22; UNNOW_1. Hyp: PS01201 protein; Complete proteome; SEQUENCE 219 AA; 24758 MW; EA30A3CDFU8683DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49566 MW; 5B5DA87E19879644 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AA.
                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09U9R1;
01-JUN-2001 (TrEMBLrel, 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-C57BL/6J; TISSUE-TESTIS;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1923275; 5830420C20Rik.
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SEQUENCE FROM N.A. MEDMed-8946165; MEDVINE-97101647; Pubmed-8946165; MEDS.INE-97101647; Pubmed-8946165; MEDVING-0010164; Uching and sequencing of a 27.8-kb nucleotide sequence of the 79 degrees 181 degrees region of the Bacillus subtilis genome containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Euxaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dakaryota: Fungi, Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998). EMBL; ALI17195; CABS5023.1; -SRQUENCE 684 AA; 79659 MW; FOE4FAF28EAFF687 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.7%; Score 30; DB 2; Length 610; 66.7%; Pred. No. 4.7e+02; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                    the sspE locus.";

DNA Res. 3:257-262(1996).

EMBL: D85082; BAA24464.1; -.

SEQUENCE 610 AA; 69089 MW; 34094DD5CA72FF66 CRC64;
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(01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
(11.UNV-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 110.7 KDA PROTEIN YDL035C.
GPRI OR D2749 OR YDL035C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%; Score 30; DB 5; I
66.7%; Pred. No. 5.3e+02;
ive 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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MENNINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-00T-2000 (TrEMBLrel. 15, 01-00T-2000 (TrEMBLrel. 15, 01-MRR-2001 (TrEMBLrel. 16, Y57A10A.20 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
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Best focal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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574 YKPEWR 579
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672 FKPKWK 677
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Q9NA80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Runst F., Ogdsawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Ravedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Ravedo V., Bertero M.G., Brash A., Braun M., Birjanell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Rolis S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., R. Entian K.D., Errington J., Fabret C., Furitta S., Galaeron N., Golightly E.J., Grandi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., R. Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., R.A. Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., R. Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., A. Levine A., Lardinois S., Lauber J., Lazarevic V., A. Moone D., O'Reilly M., Ogawa K., Ogiwara A., Lauber J., Lazarevic V., A. Porlis B., Branda S., Mauel C., Medigue C., A. Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., A. Packorska A., Seror S.J., Serror P., Shin B.S., Soldo B., Seror T., Scanlan E., Schleich S., Schroeter R., Scoffone F., A. Sorokin A., Taackoni E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Tarakahashi H., Takemaru H., Yasaarotti A., Wambutt R., Wadler E., Wadler H., Yashikawa H., Danchin A., Yasaan, C., Wallamane K., Yoshikawa H., Danchin A., Yasaan, C., Wallamane K., Yoshikawa H., Wandier E., Wallamane K., Yoshikawa H., Wandier E., Wallamane K., Yoshikawa H., Wandier H., Wandier B., Wallamane M., Wandier H., Wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the gram-positive bacterium Bacillus
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Pred, No. 4.7e+02;
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: Z9108; CAB12672.1;
COMPLETE PICLE
SEQUENCE 606 AA; 68677 MW; 4B58DD58922EDDCA CRC64
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Last annotation update)
                                                                                                                                                                                                                            Macteria; Firmicutes; Bacillus/Clostridium group;
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                                                                                                                                                                                                                                                                  Bacillus/Staphylococcus group; Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98044033; PubMed-9384377;
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                           01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                 Racillus subtilis
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570 YKPEWR 575
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                                                                                                                                       PROTEIN.
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RESULT 12 052961

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"Structural analysis of Arabidopsis Lhallana chromosome 3. II.

"Structural analysis of the regions of 4,251,695 bp covered by ninety Pl,

TAC and BAC clones.":

DNA MES. 7:217-221(2000).

-! SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

FMBL, APU00414; HAH01179.1;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GB|AAD55299.1.
Arabidopsis thaliana (Mouse-car cross).
Butaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: cudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 9.2e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Score 30; DH 3; Length 961; Pred. No. 7.3e+02; 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                              Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; %71781; CAA96454.1; -.
EMBL; 274083; CAA98593.1; -.
EMBL; 274081; CAA98593.1; -.
Hypothetical protein.
SEQUENCE 961 AA: 110708 MW; 9889D857872A4209 CRC64;
                                                     STRAIN-ALPHA S288C;
Paulin L., Saren A.M.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ dalabases.
                                                                                                                                                       Paulin L., Sarén A.M., Laamanen P.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKT; 1232 AA.
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Interpro: IRR000194: Arpase_alpha_beta.
Interpro: IRR001841: Znf_ring.
Interpro: Znf_ring.
Interpro: Znf_ring.
Interpro: Znf_ring.
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66.7%;
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Best Local Similarity 66.78;
Matches 4; Conservative
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Best Local Similarity 66.73
Matches 4; Conservative
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                                     SEQUENCE FROM N.A.
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Pubmed-10907853;
NCBI_TaxID=4932;
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156 FKPNWK 161
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SEQUENCE
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Oy 1 FKPXWR 6

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Db 9.02 FKPGWK 907

Search completed: February 27, 2002, 11:50:09
Job time: 988 sec
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C. P.ATION: 1
3 'HER INFORMATION: 2
57 HER INFORMATION: 2
67 HER INFORMATION: 2
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ANT: - SENSE: NO
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FEATURE
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Sequence 35, Appl
Sequence 9, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 13, Appli
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Sequence 2, Appli
Sequence 351, App
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Sequence 26, Appl
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                                                                                                                                        (without alignments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                        February 27, 2002, 11:36:04; Search time 132.19 Seconds
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Sequence 2
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Copyright (c) 1993 - 2000 Compugen LLd.
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US-08-079-051-2
PCT-0294-0694-2
US-08-813-974B-351
US-08-813-974B-351
US-08-118-270-35
US-08-970-35
US-08-970-1
US-08-970-1
US-08-96-616-113
US-08-96-616-113
US-08-90-612-411-113
US-08-90-612-411-113
US-08-012-431-113
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US-09-012-613-113
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US-09-461-474-14
US-08-666-3678-6
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Listing lirst 45 summaries
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Gapop 10.0 , Gapext 0.5
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28 27 77.1 566 4 US-09-143-438-5 Sequence 5, Appli 39. 27 77.1 1556 4 US-09-143-418-5 Sequence 2, Appli 3. 27 77.1 1552 4 US-09-091-219-25 Sequence 10, Appl 32. 27 77.1 2232 4 US-09-091-219-25 Sequence 21, Appl 32. 27 77.1 2247 4 US-09-091-219-2 Sequence 27, Appl 34. 26 74.3 10 2 US-08-04-65-20 Sequence 27, Appl 35 26 74.3 42 2 US-08-06-6584-27 Sequence 27, Appl 35 26 74.3 273 1 US-08-06-6584-27 Sequence 27, Appl 37 1 US-08-06-6584-27 Sequence 27, Appl 37 2 US-08-09-07-65-55-20 Sequence 27, Appl 37 2 US-08-097-362-75 Sequence 75, Appl 37 2 US-08-097-362-75 Sequence 75, Appl 37 2 US-08-097-362-75 Sequence 75, Appl 49 26 74.3 273 4 US-09-095-855-75 Sequence 75, Appl 41 26 74.3 370 2 US-08-097-862-75 Sequence 75, Appl 41 26 74.3 370 2 US-08-097-862-75 Sequence 194, Appl 44 26 74.3 370 2 US-08-097-862-194 Sequence 194, Appl 44 26 74.3 370 2 US-08-097-862-194 Sequence 194, Appl 44 26 74.3 370 1 US-09-095-852-194 Sequence 194, Appl 44 26 74.3 417 1 US-08-351-981-6
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ALIGNMENTS

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/label- BH
/note= "either the natural phenylalanine amino
terminus or the Holton-Hunter modified peptide
Sequence 13, Application US/08215137
Patent No. 5614370
GENERAL INFORMATION:
GENERAL INFORMATION:
A-PLICANT: Stochiano, Salvatore J
A-PLICANT: Springer, Martin S
THE OF INVENTION: ASSAT TO IDENTIFY HUMAN C5A ANTAGONISTS
WITHER OF ENVENTION: AND AGONISTS
WITHER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                           AUDRESSEE: Merck & Co., Inc.
STREET: 126 Linclon Ave., P.O. Box 2000
CITY: Rahway
                                                                                                                                                                                                                                                               Cift: Rahway
STATE: New Jersey
CHITE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New LICATION NUMBER: US/08/215,137
P.T.ING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAAE: Benten, Gerard H
REJISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 19108
PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WOTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (908) 594-4720 INPORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "RAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i amino acids
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RICSCULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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. 1 | 1 | 4 WKPKWR

OTHER INFORMATION: having the group 3-(p-hydroxypenyi)propionyl group

NAME/KEY: Modified-site

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DB 1; Length 16;
10;
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TITLE OF INVENTION: ANTIBODIES TO HUMAN C5a RECEPTOR
NUMBER OF SEQUENCES: 4
                                                                                                                                      APPLICANT: EMBER, JULIA A.
APPLICANT: HUGLL, TONY E.
TITLE OF INVENTIONS ANTIBODIES TO HUMAN C5a RECEITION
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horu Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/ACENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2790
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/079,051
FILING DATE: 18-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9406994 GENERAL INFORMATION:
                                            US-08-079-051-2
; Sequence 2, Application US/08079051
; Patent No. 5480974
                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEUIUM TYPE: Floppy disk
COMPUTER: I'BM PC COMPATIBLE
                                                                                                 GENERAL INFORMATION:
APPLICANT: MORGAN, EDWARD L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS: LENGTH: 16 amino acids
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOURCULE TYPE:
                                                                                                                                                                                                                                                                                                                        69006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-079-051-2
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                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                    STATE:
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                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erile, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THEATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
O
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                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                              Length 6;
                       /label- dCha
/note= "D-cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                          Score 33; DB 1; L
Pred. No. 1.6e+05;
0; Mismatches 0;
                                                                                                                 /label- dArg
/note- "D-arginine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: No. 6180604 tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317 REFERENCE/DOCKET NUMBER: 660081.405 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/915,314
FILING DATE: 20-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
                                                                                                                                                                                                     94.3%; Scor
100.0%; Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                          NAME/KEY: Modified-site
LOCATION: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206) 682-6031
INFORMATION FOR SEQ 1D NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7'
Matches 4: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 amino acids
                                                                                                                                                                                                                                               Conservative
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LOCATION: 4
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                           COCATION: 6
CTHER INFORMATION:
CTHER INFORMATION:
US-08-215-137-1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
: USA
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                                                                                                                                                                                                                            Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 20
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seattle
                                                                                                                                                                                                                                                                                                        1 FKPXWR 6
                                                                                                                                                                                                                                                                                   1 FKPXWR 6
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III. Surya K.

III.E OF INVENTION: NOVEL REGULATORS OF G-PROTEIN
TITLE OF INVENTION: SIGNALING
ALMSTR OF SEQUENCES: 6
FORTHSTROME ADDRESS:
FORTH
                                                                                                                                                                                                  PRICING DATE: 16 MAR. 1995
PRICING DATE: 16 MAR. 1995
PRICING DATE: 20-JAN-1995
PRICING DATE: 20-JAN-1995
PRICING DATE: 20-JAN-1995
PRICING DATE: 20-JAN-1995
PRICING DATE: 28-DEC-1994
PRICING DATE: 28-DEC-1994
PRICING DATE: 28-DEC-1994
PRICING DATE: 30-NOV-1994
PRICING DATE: 30-NOV-1994
PRICING DATE: 30-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 6-189274
PILING DATE: 11-AUG-1994
PHION REPLICATION DATA:
PILLING DATE: 11-AUG-1945
PILLING DATE: 11-AUG-1945
PILLING DATE: 11-AUG-1945
PILLING DATE: 11-AUG-1994
APPLICATION NUMBER: JP 6-189272
PILLING DATE: 11-AUG-1994
APPLING DATE: INFORMATION:
                                                                                                                                                                           IMBER: JP 7-057186
16-MAR-1995
                                                                                     JP 7-093989
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Paten: No. 5882390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAME: Resnick, David S. ARCISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 351: SEQUENCE CHARACTERISTICS: LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: 78LEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 80.0%;
Matches 4; Conservative
                                                                               APPLICATION NUMBER: JP 7-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           517-523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOOLOGY: linear NOUSCULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 30-SEP-1
                       FILING DATE: 10-AUG-
                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CTY: Path Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-513-974B-351
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C
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APPLICANT: FUJII, RYO
APPLICANT: FUJII, RYO
APPLICANT: Obtaki, Tetsuya
APPLICANT: Objai, Kazuhiro
APPLICANT: Objai, Kazuhiro
TITLE OF INVENTION: G PROTEIN COUPLED RECEFTOR PROTEIN,
TITLE OF INVENTION: 3800
NUMBER OF SEQUENCES: 380
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130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DOS
SOFTWARE: Patentin Release #1.0. Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06994 FILING DATE: 20-JUN-1994 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/UB/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/ACENT INFORMATION:
NAME:::Tumarkin, Lisa A
REGISTRATION NUMBER: P10-2790
REFERENCE/NOCKET NUMBER: F10-2790
TELEPHONE: (619) 455-5100
TELEPRAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 351, Application US/08513974B Patent No. 6114139
                                                                                                             COMPUTER: FBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.0%;
80.0%;
                                                                                     Floppy disk
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Hosoya, Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 80.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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ADDRESSEE: DIKE, BRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C5aR(133-148)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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APPLICANT: Hinuma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
PCT-US94-06994-2
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COUNTRY:
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Sequence 35, Application PC/TUS9308528
CENERAL INFORMATION:
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CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL OF INVENTION:
CENERAL OF INVENTION:
CENERAL OF INVENTION:
CENERAL OF INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSE:
CORRESPONDENCE ADDRESS:
ADDRESSE:
CENERAL OF INVENTION:
CENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: 16M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SUBRET APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
FRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.0%; Score 28; DB 5; 1
80.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB 1;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Townsend, Kevin G.
PEGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MUKPHY=2 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTER(STICS:
   REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION
TELEPINE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.0%;
                                                                                                                                                                                                              LENGTH: 304 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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Best Local Similarity 80.0.
                                                                                                                        TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DD .103 FKPIW 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
CORRESPONDENCES: 344
ADDRESSEE: HROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 243;
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COMPUTER: IRM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
IMBIOR PUBLICATION DATA:
APPLICATION NUMBER: US 07/943,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 2; I
Pred. No. 1.5e+02;
0; Mismatches 1;
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                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J.
RECISTRATION NUMBER: 36,749
REFERENCE/TOCKET NUMBER: PF-0259 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/829,110
FILING DATE: Filed Herewich
FILING STATION: 514
PRIOR APPLICATION: 514
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35, Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
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ATTORNEY AGENT INFORMATION:
MAKE: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                  IBM Compatible
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 243 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskell
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                                                                                                                                                 OPERATING SYSTEM:
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LIBRARY: THIMMEDIBLE 343504
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                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 11
71 KPAWR 75
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COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20004
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COUNTRY:
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Cength 463;
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                                                                                                                                                          SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DAYA:
APPLICATION NUMBER: US/09/082,310
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28; DH 3; Pred, No. 2.9e+02; U; Mismatches D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CHRYCHT APPLICATION DATA: ASPLICATION NUMBER: US/08/876,874
                                                                                                                                                                                                                                                                 ANTURNEY/AGENT INFORMATION:
NAME: FERRONE, MICHAEL C.
REGISLASTION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0520 US
TELECOMMUNICATION INFORMATION:
                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 2, Application US/08876874; Patent No. 5942405; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.08;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bergsma, Derk
APPLICANT: Foley, James
APPLICANT: Kumar, Chandrika
APPLICANT: Sarau, Herri
                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *: AMPUTER: IRM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AuptiCANT: Ames, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 536
PRICH APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: P.O. BOX 980
CLPY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: SADIUM TYPE: Diskett
                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
PALO ALTO
CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: slu
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Matches 4; Conserv
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                                             USA
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293 KPSWR 297
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                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: We, Henry
TTTLE OF INVENTION: HUMAN NUCLEIC ACID METHYLASES
NUMHER OF SEQUENCES: 4
COMMESSORING ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 2; Pred. No. 2.2e+02;
                                                                                                                                                                                  APPLICANT: LI, ET AL.
TITLE OP INVENTION: C5a Receptor
NUMBER OF SEQUENCES: 11
CORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEMARY 6 OLSTEIN
STREFT: 6 HECKER FARM ROAD
CITY: ROSFLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REGIABLE FURM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 1 HM PS/2
OPPERTING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,970A
FILING DATE: JUNE 2, 1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,073
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: June 2, 1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: PCT/US94/09234
FILING DATE: 16 AUG 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                      Sequence 9, Application US/08458970A
Patent No. 5861272
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09082310 Patent No. 6096526
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 350 amino acids TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Hest Local Similarity 80.0
المحمد 4; Conservative
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; MOLECULE TYPE: protein
US-08-458-970A-9
                                                                                                                                                                                                                                                                                                                                                     STATE: NEW JERSEY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 |
139 FKPIW 143
    111 |
103 FKPIW 107
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                                                                                   RESULT 9
US-08-458-970A-9
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Patent No. 6121035
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rushlow, Keith E.
APPLICANT: Frank, Glenn R.
APPLICANT: Frank, Glenn R.
APPLICANT: Stingelor, Gary
APPLICANT: Stiver, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
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O
                                                                                Length 496;
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                                                                                                                      1; Indels
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CURRENT APPLICATION DATA:
PALICATION NUMBER: US/08/906,616
FILING DATE: 05-AUG-1997
                                                                              Score 28; DB 3; 1
Pred. No. 3.1e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.1e+02;
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Pred. No. 3.1e+0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sheridan Ross P.C.
1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-8:7-795-113; Sequence 113; Application US/088177.95; Packent No. 6139840; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: CONNES!, Gary J.
REGISTATION NUMBER: 32,020
REFRENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
FELEPHONE: (303) 863-9700
                                                                                                                      .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.0%;
80.0%;
                                                                              80.0%;
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                      Conservative
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      : MOLECULE TYPE: protein
US-08-906-769-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                              Ouery Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colorado
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Denver
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358 FKPKW 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 FKPXW 5
                                                                                                                                                        FKPXW 5
                                                                                                                                                                                                                                                                        US-08-906-616-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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APPLICANT: Grieve, Robert B.
APPLICANT: Wushlow, Keith E.
APPLICANT: Frank, Glean
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Silver, Gary
TITLE OF INVENTION: FIEB PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                   Lenyth 482;
                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-100S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,769
                                                                                                                                                                                                                                                                                                                                             80.0%; Score 28; DB 2;
80.0%; Pred. No. 3e+02;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: CONDETT, GATY J.
KEGISTRATION NUMBER: 32,020
KERENCE/DOKET NUMBER: 2618-25-C2
TELECOMMUNICATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24.APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 113, Application US/08906769
Patent No. 6077687
GENERAL INFORMATION:
                                                          P50501
                  NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/TOCKET NUMBER: P505
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEFAX: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ 1D NO: 113:
                                                                                                            TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ 1D NO: 2:
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acids
TYPE: amino acid
STANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                             Ouery Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
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US-08-876-874-2
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125 FKPIW 129
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CORRESPONDENCE ADDRESS:
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                                                          APPLICANT: HEACH, Andrew W.
APPLICANT: HEACH, Andrew W.
APPLICANT: HEACH, Andrew W.
APPLICANT: Argen, Miles Yamanaka
APPLICANT: Argen, Miles Yamanaka
APPLICANT: Argen, Andrew W.
APPLICANT: Bale, Beverly
APPLICANT: Stleder, Gary
TITLE OF INVENTION: USE OF PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: INFESTATION, AND FLEA PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: MOLECULES, AND SES THEREOF
CORRESPONDENCES: 119
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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TITLE OF INVENTION: FLEA PROFEASE PROFEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 80203
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: PROPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTER RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Sequence 113, Application US/08639075A
; Patent No. 6150125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grieve, Robert B.
Rushlow, Keith E.
Wu Hunter, Shirley
Frank, Glenn R.
Stiegler, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECISTRATION NUMBER: 32,020 REFERENCE/INCRET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wu Hunter, Shirley
APPLICANT: Frank, Glenn R.
APPLICANT: Stiegler, Gary
APPLICANT: Gaines, Palrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (303 863-0223 INFORMATION FOR SEQ ID NO: 113:
                                              unter, Shirley Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (303) 863-9700
(303 863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
TYPE: amino acid
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Best Local Similarity 80.0
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-817-795-113
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                                                                                                                                                                                                                                                                                                                                                                                          CITY: Denver
STATE: Colorado
COUNTRY: USA
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APPLICANT: Grieve,
APPLICANT: RUShlow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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358 FKPKW 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
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US-08-639-075A-113
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/639,075A
FLIING DATE: 24-APR-1996
CLASSIFICATION: 424
ATTORREY/AGENT INFORMATION:
NAME: COUNCIL, GARY 32,020
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 32,020
REGISTRATION NUMBER: 36,023
INFORMATION: (303) 863-9700
TELEPHONE: (303) 863-9700
TELEFRAX: (303) 863-923
INFORMATION: ECR SEO ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENTH: 496 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%; Score 28; DB 4; I
80.0%; Pred. No. 3.1e+02;
Live. 0; Mismatches 1;
ADDRESSER: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February'27, 2002, 11:36:04 Job time: 143 sec
                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Eocal Similarity 80.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                               CITY: Denver
STATE: Colorado
COUNTRY: USA
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February 27, 2002, 11:41:15; Search time 303.5 Seconds (without alignments) 1.464 Million cell updates/sec
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/SIDSB/gcgdata/genescq/geneseqp/AA1993.
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/SIDSB/gcgdata/geneseq/geneseqp/AA1995.
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/SIDS8/gcgdata/geneseq/geneseqp/AA1991
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: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.
:: /SIDS8/gcgdata/geneseqp/AA1981.
GenCore vorsion 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522463 seqs, 74073290 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Listing first 45 summaries
                                                                                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Match Length DB
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Human myotonic dys Newcastle disease Human colon cancer Human colon cancer Amino acid permeas Indolicidin analog Indolicidin analog Indolicidin analog Cationic peptide o Amino acid sequenc Amino acid sequence Am	Hunt acreted pro Arabidopsis thalia 2ea mays protein f
AAK41001 AAK51233 AAB53398 AAB53398 AAB572313 AAB572313 AAR6370 AAW66370 AAW66370 AAW66370 AAW66370 AAW66370 AAW66370 AAW66370 AAW20300 AAR179002 AAR179002 AAR179002 AAR179002 AAR179002 AAR179002 AAR179002 AAR179002 AAR179002 AAR179003 AAR17903	AAG03517 AAG10416 AAG40668
41122222222222222222222222222222222222	21 21 21 21 21 21 21 21 21 21 21 21 21 2
22043 22044 2190 2190 2190 2193 2193 2193 2193 2103 2103 2103	126 128 128
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50046667 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	: दग र : दगर

ALIGNMENTS

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Anaphylatoxin; receptor; ligand; antlinflammatory; hexapeptide; neprapeptide; immunodeficiency; allergy; autoimmune; ARDS; cancer; influstion; endotoxin; asthma; gout, psoriasis; cirrhosis; inflammatory; bowel; disease; hepatitis; burns; myocardial; infarction; transplant rejection; ischaemic.
                                                                                                                                                                                                                                                                                 'note" "(2R)-2-amino-3-cyclohexyl-propanoyl"
                                                                                               Muaphylatoxin antagonist or agonist peptide.
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                            /note= "N-Me-Phe"
                     A.16.30577 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                         /note= "D-Arg'
                                                                                                                                                                                                                                                                     /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                  91WO-US09319.
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                                                                     (first entry)
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                                                                                                                                                                                                                                                                                              Modified-site
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AAY58358 AAY58356 AAY58357 AAY58357

AAB01208 AAG98875 AAY58359 AAY58360

AAR30577 AAR89737 AAW74031

Anaphylatoxin anta C5a peptide analog Human D2H binding ~

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Claim 2; Page 54; 294pp; English
                                                                                                                                                                                                                                                                  Conservative
          (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELAN-) ELAN CORP PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CYTO-) CYTOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-009568/01
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Best Local Similarity
Matches 6: Conserv
                                                                                                                                                                                                                                                                                     1 FKPXWR 6
                                                                                                                                                                                                                                                                                                        1 fkpxwr 6
                               Konteatis 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9851325-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 - MAY - 1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Omahony DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alvarez VL,
                                                                                                                                                                                                                                                                                                                                                                               AAW74031;
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                  AAW7403]
                                                                                                                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                          The peptide is a specifically claimed example of a group of highly generic hexa- and heptapeptides which are (a) anaphylatoxin antagonists useful for tracting asthma, other allergies, inflammations, autoimmune diseases, serum sickness, gout, bullous skin diseases, psoriasis, RRDS, endotoxin shock, hepatic cirrhosis, pancreatitis, inflammatory bowel disease, burns, sepsis, myocardial infarction, chronic hepatitis, transplant rejection, or ischaemic heart or brain damage; or (b) anaphylatoxin agonists useful for stimulating inflammatory and immune responses, e.g. in the treatment of cancer, immunodeficiency diseases and severe infections.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C5a: complement; agonist: antagonist; peptide; binding assay; identification; inflammation; pain reduction; respiratory disorder; cardiovascular; hypertension; ARDS; anaphylaxis; arthritis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label* Phe, OTHER /note* "OTHER * the Bolton Hunter modified peptide having the 3-(p-hydroxyphenyl)-propionyl
                                                                 New hexa- and hepta:peptide(s) are anaphylatoxin antagonists and agonists - for treating inflammatory and immunodeficiency diseases, cancers and severe infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   C5a peptide analogue, C089, used to identify C5a (ant)agonists.
                                                                                                                                                                                                                                                                          Length 6;
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                            Wagner R, Wiedeman PE;
                                                                                                                                                                                                                                                                         DB 13; L
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6
                                                                                                                                                                                                                                                                       94.3%; Score 33; DB 100.0%; Pred. No. 4.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                         Claim 11; Page 153; 160pp; English,
                                                                                                                                                                                                                                                                                                                                                                                       AAR89737 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- OTHER
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        (ABBO ) ABBOTT LABORATORIES
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                            Or YS,
                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 6; Conservative
                                               WPI; 1992-268383/32
                            Luly JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     competitive
                           Kawai M,
                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D2H; hPEPT1; human; GI tract receptor; sucrose-isomaltase complex; intestinal peptide-associated transporter; hypertension; diabetes; osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                  C5s receptor binding assays : used for identifying cpds.having C5a antagonist, agonist or partial agonist activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gastro-intestinal transport receptor; binding protein; hSI; HPTl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimaeras and antibodies, used to deliver therapeutic or diagnostic agents to, through, the gastrointestinal tract, e.g. insulin or leuprolide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.3%; Score 33; DB 16; I. 100.0%; Pred. No. 4.3e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cagney GM, Carter JM, Singleton J;
   Springer MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic agent delivery; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW74031 standard; peptide; 39 AA.
                                                                                                                                                                                                                                              Claim 15; Page 47; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human D2H binding protein DAB3.
Siciliano SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Belinka BA, Ca
Patterson CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US10088
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This sequence represents a peptide that specifically binds to the human D2H protein. The invention relates to putified proteins (I) that bind specifically to at least one of the gastro-intestinal (GI) tract receptors human intestinal peptide associated transporter (HPT1).

The following transport of therapeutic agents through human and animal GI tissue active transport of therapeutic agents through human and animal GI tissue (into the blood) for in vivo delivery, particularly for treatment or prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia, CC anner, migraine, or angina pectoris. Specifically they are used to deliver, insulin or leuprolide, but many other suitable therapeutic agents are disclosed, including genes or inhibitory nucleic acid, imaging agents and antiques. (I) may also provide targeting to the GI tract. Other uses CC of (I) arc: (i) to determine the level of specified receptors in a sample CC and antiques. (i) to determine the level of specified receptors in a sample CC Immunogenic analogues or derivatives of (I) are used to raise antibodies are used to locate, detect and mad in immunoassays. The antibodies are used to locate, detect and measure (I), e.g. for imaging, monitoring treatment, tissue analysis cute., also for peptide purification and immobilisation.

39 AA; Sequence

Gaps .; O Score 30; DB 20; Length 39; Pred. No. 18; 1; Mismatches 1; Indels 85.7%; 66.7%; 4; Conservative Best Local Similarity Matches 4; Conser Query Match

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15 frpgwr 20

AAB01208 standard; Protein; 434 AA. AAB01208;

12-DEC-2000 (first entry)

Corn putative lecithin:cholesterol acyltransferase #3.

Corn; lecithin:cholesterol acyltransferase: phytosterol: phosphatidylcholine-sterol O-acyltransferase; heat shock; cold shock.

Zea mays.

WO200032791-A2.

08-JUN-2000

02-DEC-1999;

98US-0110782 03-DEC-1998;

99WO-US28586

(DUPO) DU PONT DE NEMOURS & CO E I.

Butler KH, Saylor JJ; Sakai H, Shen JB, Kinney AJ, Cahoon RE,

WPE; 2000-412337/35. N-PSDB; AAA49203 Polynucleotide encoding plant lecithin; cholesterol acyltransferase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening CDNA expression Libraries

Claim 10; Page 40-41; 49pp; English.

The present sequence is a putative protein sequence of a corn lecitiniciolesterol acylicansferase (also known as phosphatidylcholine-storol Ocacylicansferase). This enzyme is found associated with high-density lipoproteins and Apolipoprotein-Al and -D. RESULT
AAB01208
XX
AAB01208
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AAB0
DT 12-DI
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X

clusted DNA sequences (I). AAH84500 to AAH84670 encode the E. collated DNA sequences (I). AAH84500 to AAH84670 encode the E. coll sequences (I). AAH84500 to AAH84670 encode the E. coll sequences (I). AAH84500 to AAG9909 and AAG9908 and AAG9909 an ö The gene and protein can be used to produce transgenic plants which have increased lipid metabolism and membrane fluidity, and therefore increased resistance to heat and/or cold shock, to alter the content of phytosterol or lecithin in grains and to identify potential herbicides. coli growth and proliferation related protein sequence SEQ ID NO:345. For all nucleic acids that inhibit Escherichia coli proliferation, useful for screening for homologous genes and for designing expression vectors so screen for specific microorganisms that produce such proteins in a specifies specific manner. AAHB4371 and AAHB4470 represent sequencing primars used in the isolation of E. coli growth and proliferation contained sequence, which are used in an example from the present Gaps Escherichia coli; growth; proliferation; microbial; antimicrobial; bacterial infection; microorganism. ö Length 434; 1; Indels Score 30; DB 21; Pred. No. 2.1e+02; 1; Mismatches 1; Clean 19; Page 421-422; 522pp; English. AAC98875 standard; Protein; 462 AA. Ohlsen K, Zyskind J; 85.7%; 66.7%; UN NOV-2000; 2000WO-US30950 99US-0164415 26-SEP-2001 (first entry) Conservative (BUELT'S BLEERA PHARM INC. Quer; Match Best Local Similarity The 4; Conserve KPZ: 2001-335933/35 434 AA; Escaerichia coli. V-7.30B; AAH84546 1:1 | 1: 271 frpmwr 276 W0200134810-A2 33-NOV-1999 FKPXWR 6 Prisvth RA. 17 - MAY - 2001 AAG98875; Sugrence AAG98875 2000238 Š S

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Gaps

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Score 30; DB 21; Length 700; Pred. No. 3.5e+02;

85.7%;

700 AA;

1; Mismatches

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156 fkpnwk 161
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     Sequence
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                                                    Ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel yeast G protein-coupled receptor,

CPR1 (AAY58355). GPR1 is predicted to have seven transmembrane domains,
which is characteristic of G protein-coupled receptors, and also
contains a very large third cytoplasmic loop and a large cytoplasmic

tail. The third cytoplasmic loop contains two short basic sequences: one
sequence (KRRRAQIO) is present at the N-terminal end of the loop and the
cytoplasmic loop also contains an asparagine-rich region. GPR1 is
believed to provide the upstream signal that activates GPA2, and plays
believed to provide the upstream signal that activates GPA2, and plays
an essential role in inducing the switch from non-filamentous to
illamentous growth in yeast. Modulators of GPR1 function, especially
inhibitors, are useful for prevention or treatment of a disease or
inscrted heterologous sequence inactivates the biological activity of
control of the modulate GPR1 gene expression and/or gene product
control of the modulate GPR1 gene expression and/or gene product
control of the modulate GPR1 gene expression and/or gene product
control of the modulate GPR1 gene expression and/or gene product
control of the inhibit the conversion of a fungus from a
non-filamentous form to a filamentous form. The present sequence
control of the inhibit the modulate GPR1
con-filamention. This sequence is lacking the majority of the cytoplasmic
conversion of a fungus from a conversion of a fungus from a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel protein, gene, antibody and recombinant cell useful for identifying modulators and inhibitors useful as anti-fungals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from the yeast GPR1 amino acid sequence given in figure 1A.
                                                                               Length 462;
                                                                           Score 30; DB 22; Length 46
Pred. No. 2.3e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                       Yeast G protein-coupled receptor GPR1 mutant d694-954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6.2.5; Page -; 63pp; English.
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                                                                                                                                                                                                                                                       AAY58359 standard; Protein; 700 AA.
                                                                             85.7%;
66.7%;
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                                                              Ouery Match
Best Local Similarity 60...
Best Local 4: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-086980/07
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                               462 AA;
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398 ykplŵr 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
 invention.
                                                                                                                                                                                                                                                                                         AAY58359;
                                 Sequence
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The invention relates to a novel yeast G protein-coupled receptor, CPRI (AAYS835). GPRI is predicted to have seven transmembrane domains, which is characteristic of G protein-coupled receptors, and also contains a very large third cytoplasmic loop and a large cytoplasmic copy contains two short basic sequences: one sequence (KRIKAOIG) is present at the N-terminal end of the loop and the cytoplasmic loop contains an apparagine-rich region. GPRI is believed to provide the upstream signal that activates GPA2, and plays an essential role in inducing the switch from non-filamentous to filamentous to filamentous are useful for prevention or treatment of a disease or filamentous growth in yeast. Modulators of GPRI function, especially inhibitors, are useful for prevention or treatment of a disease or disciplinational activity may be used to inhibit and activity of current and plays are included which modulate GPRI gene expression and/or gene product curvity may be used to inhibit the conversion of a fungus from a non-filamentous form to a filamentous sequence. Conversion of a fungus from a non-filamentous form to a filamentous down the presents a GPR mutant, d277-284, used in an exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     native GPRÍ.
Note: This sequence is not shown in the specification, but is derived
from the yeast GPRI amino acid sequence given in figure IA.
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                                                                                                                                                                                                                                                                                                                                                       Yeast, G protein-coupled receptor, GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mulein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel protein, gene, antibody and recombinant cell useful for identifying modulators and inhibitors useful as anti-fungals
                                                                                                                                                                                                                                                                        Yeast G protein-coupled receptor GPR1 mutant d841-954.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUN ) MOUNT SINAI SCHOOL MEDICINE
AAY58360 standard; Protein; 847 AA.
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                                                                                                                                                                                (first entry)
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Synthetic.
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Gaps

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The invention relates to a novel yeast G protein-coupled receptor, C CPRI (AAY$335). Great is predicted to have seven transmembrane domains, which is characteristic of G protein coupled receptors, and also contains a very large third cytoplasmic loop and a large cytoplasmic sequences; one tail. The third cytoplasmic loop contains two short basic sequences; one sequence (KRRAAOIG) is present at the N-terminal end of the loop and the other sequence (KRRAAOIG) is at the C-terminal end of the loop and the other sequence (KRRAAOIG) is at the C-terminal end of the loop. The third cytoplasmic loop also contains an asparagine-rich region. GPRI is believed to provide the upstream signal that activates GPA2, and plays an essential role in inducing the switch from non-filamentous to tilamentous growth in yeast. Modulalors of GPRI function, especially inhibitors, are useful for prevention or treatment of a disease or disorder involving a fungal infection. The inhibitor may be an anti-GPRI antibody, GPRI antisense nucleic acid or a GPRI gene altered so that an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inserted heterologous sequence inactivates the biological activity of GPR1. Compounds which modulate GPR1 gene expression and/or gene product activity may be used to inhibit the conversion of a fungus from a non-tilamentous form to a fillamentous form. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: This sequence is not shown in the specification, but is derived from the yeast GPR1 amino acid sequence given in figure 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to invention. This sequence is lacking the asparagine-rich region the third cytoplasmic loop, relative to the native GPR1.
                                                                                                                                                                                                                                                                                                                                                                                           Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form: signalling pathway; antifungal; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents a GPR mutant, d277-284, used in an exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel protein, gene, antibody and recombinant cell useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dentifying modulators and inhibitors useful as anti-fungals
Score 30; DB 21; Length 847; Pred. No. 4.2e+02; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                    Yeast C protein-coupled receptor GPR1 mutant d490-586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6.2.5; Page -; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOUN ) MOUNT SINA! SCHOOL MEDICINE.
                                                                                                                                                                                                                               AAY58358 standard; Protein; 864 AA.
  85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US11838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0088311
                                                                                                                                                                                                                                                                                                              27-MAR-2000 (first entry)
                                          4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-086980/07
    Query Match
Best Local Similarily
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirsch JP, Xue Y;
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                                                                                                                         156 fkpnwk 161
                                                                                   1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9963094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-1999;
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The invention relates to a novel yeast G protein-coupled receptor,

"The invention relates to a novel yeast G protein-coupled receptors,

"The invention is characteristic of G protein-coupled receptors, and also
"Antal is characteristic of G protein-coupled receptors, and also
"Antal is characteristic of G protein-coupled receptors, and also
"Antal is characteristic loop contains two short basic sequences; one
sequence (RRIKAQIG) is present at the N-terminal end of the loop and the
"The third cytoplasmic loop also contains an apparagine-rich region. GPR is
"The couple of the upstream signal that activates GPA2, and plays
an essential role in inducing the switch from non-filamentous to
"Ilamentous frowth in yeast. Modulators of GPRI function, especially
Inhibitors, are useful for prevention or treatment of a disease or
"Isakerder involving a fungal infection. The inhibitor may be an anti-GPRI
cativity may be used to inhibit the conversion of a fungus from a
non-filamentous form to a filamentous form. The present sequence
"Secretary of a filamentous form to a non-filamentous form to a filamentous form. The present sequence
"Secretary invention. This sequence is lacking the first basic motif (KRIKAQIG)
"The third cytoplasmic loop, relative to the native GPRI
"Note: This squence is not shown in the specification, but is derived
"The trian and a squence given in figure lA."
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                                        Gaps
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Pred. No. 4.3e+02;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                       Yeast G protein-coupled receptor GPR1 mutant d277-284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6.2.5; Page -; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AUUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                                                                          AAY58356 standard; Protein; 953 AA.
 85.7%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0088311.
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                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae.
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421, 2000-086980/07
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kirsch JP, Xue Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     953
                                                                                                 ||| |:
|56 fkpnwk 151
                                                                         J. FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09963094-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 - MAY - 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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                                                                                                                                                                                                                                               AAY58356;
   Query Match
                                        Mat: has
                                                                                                                                                                                        AAY58356
                                                                                                                                                                         RESULT
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Length 953;

Score 30; DB 21; Pred. No. 4.7e+02;

85.7%;

Que y Match Best Local Similarity

us-09-446-109a-9.rag

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i FKPXWR 6
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                                                                                                       AAYS8355
ID AAYS
                                 qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a novel yeast G protein-coupled receptor.

GPR1 (AAV$8355). GPR1 is predicted to have seven transmembrane domains, which is characteristic of G protein-coupled receptors, and also contains a very large third cytoplasmic loop and a large cytoplasmic to the loop and a large cytoplasmic sequence (KKRKAOIG) is present at the N-terminal end of the loop and the other sequence (KKRRAOIG) is at the C-terminal end of the loop and the third cytoplasmic loop also contains an asparagine-rich region. GPR1 is believed to provide the upstream signal that activates GPA2, and plays an essential role in inducing the switch from non-filamentous to flamentous growth in yeast. Modulators of GPR1 function, especially inhibitors, are useful for prevention or treatment of a disease or disorder involving a tungal infection. The inhibitor may be an anti-GPR1 intended beterologous sequence inactivates the biological activity of GPR1 compounds which modulate GPR1 gene expression and/or gene product activity may be used to inhibit the conversion of a fungus from a non-filamentous form to a filamentous form to a filamentous form to a filamentous form to a filamentous form the second basic motification of the third cytoplasmic loop, relative to the native GPR1.

KKRRAOIO) of the third cytoplasmic loop, relative to the native GPR1.

Note: This sequence is not shown in the specification, but is derived from the yeast GPR1 amino acid sequence given in figure lA.
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   Gaps
                                                                                                                                                                                                                                                                                        Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel protein, gene, antibody and recombinant cell useful for identifying modulators and inhibitors useful as anti-fungals
   Indels
                                                                                                                                                                                                                                                      Yeast G protein-coupled receptor GPR1 mutant d610-617.
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 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
                                                                                                                                                  AAY58357 standard; Protein; 953 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US11838
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 4; Conservative
                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-086980/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          953 AA;
                                                       ||| |:
|56 fkpnwk |61
                                1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                          W09963094-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                              39-DEC-1999.
                                                                                                                                                                                    AAY58357;
                                                                                                                                                                                                                                                                                                                                                            Synthetic
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                                                                                                                  RESULT 10
Matches
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Yeast; G protein-coupled receptor; GPR1; filamentous growth; pseudohyphal form; signalling pathway; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Intracellular C-terminus"
                                                                                                                                                                        /note= "Extracellular N-terminus"
                                                                                                                                                                                                                                                                                                                                                                           "Basic motif 1 (KRIKAQIG)"
                                                                                                                                                                                                                                                                                                                                                                                                            "Basic motif 2 (KKRRAQIQ)"
                                                                                                                                                                                        "Transmembrane domain 1"
                                                                                                                                                                                                             /note- "Transmembrane domain 2"
                                                                                                                                                                                                                                                                                                                                                                                             "Asparagine-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                            "Transmembrane domain 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Transmembrane domain 7"
                                                                                                                                                                                                                                                           domain 3"
                                                                                                                                                                                                                                                                                         "Transmembrane domain 4"
                                                                                                                                                                                                                                                                                                                           /note= "Transmembrane domain 5"
                                                                                                                                                                                                                             /note= "Extracellular loop 1"
                                                                                                                                                                                                        /note= "Intracellular loop 1"
                                                                                                                                                                                                                                                                                                          "Extracellular loop 2"
                                                                                                                                                                                                                                                                                                                                                           "Intracellular loop 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Extracellular loop 3"
                                                                                                                                                                                                                                                                          "Intracellular loop 2"
                                                                                                                                                                                                                                                                                                                                         /note= "Encoded by AGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Encoded by AGC"
                                                                                               reast G protein-coupled receptor GPR1.
                                                                                                                                                                                                                                                          "Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOUN' SINA! SCHOOL MEDICINE.
                                                                                                                                                        Location/Qualifiers
                                             AAY58355 standard; Protein; 961 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0088311
                                                                                                                                                                                                                                                                                                                                                                   . 284
                                                                                                                                        Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                  ..180
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                                                                                                                                                                                                                                                                                                                                                  277..620
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                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
. ||| |:
1.56 fkpnwk 161
                                                                              27 - MAR - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01 - JUN-1998;
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Gaps

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Score 30; DB 21; Length 953; Pred. No. 4.7e+02; 1; Mismatches 1; Indels

85.7%; 66.7%;

4; Conservative

Query Match Best Local Similarity Matches 4; Conserva

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contains a very large third opposite according to the contains a very large third opposite according to the contains a very large third expopasmic loop contains two short basic sequences; one sequence (KKRRAQIG) is present at the N-terminal end of the loop and the other sequence (KKRRAQIG) is at the C-terminal end of the loop. The third extoplusmic loop also contains an asparagine-rich region. GPRI is believed to provide the upstream signal that activates GPA2, and plays an essential role in inducing the switch from non-filamentous to linamentous growth in yeast, Modulators of GPRI induction, especially inhibitors, are useful for prevention or treatment of a disease or disorder involving a fungal infection. The inhibitor may be an anti-GPRI
                                                                                                                                                                                                                                                                                                                                                                                antibody, GPR1 antisense nucleic acid or a GPR1 gene altered so that an inserted heterologous sequence inactivates the biological activity of GPR1. Compounds which modulate GPR1 gene expression and/or gene product activity may be used to inhibit the conversion of a fungus from a
                                                                                                                                                      This sequence represents a novel yeast G protein-coupled receptor, GPR1. GPR1 is predicted to have seven transmembrane domains, which is:characteristic of G protein-coupled receptors, and also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "encoded by predicted reading frame a, x's in the sequence indicate stop codons in the reading frame"
                                                                Novel protein, gene, antibody and recombinant cell useful for identifying modulators and inhibitors useful as anti-fungals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30; DB 21; Length 961; Pred. No. 4.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abnormality; muscular dystrophy; CHR 19; chromosome 19; protein kinase; polymerase chain reaction; brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-filamentous form to a filamentous form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human myotonic dystrophy gene protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR41001 standard; Protein; 1093 AA.
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                                                                                                                     Claim 4; Fig 1A; 63pp; English
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66.78;
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              WPI; 2000-086980/07
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Matches 4; Conserv
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                                 N-PSDB; AAZ55699
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|56 fkpnwk 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      end of the genome of avian paramyxovirus allowing the generation of an infectious copy of avian paramyxovirus. The cell line is useful for with production of infectious lentogenic NDV (Newcastle Disease virus) without the addition of exogenous proteolytic activity. Also it is possible to generate a stable transfected cell line that expresses the wild-type F protein in the virus envelope therefore providing infectious particles, useful in the form of a vaccine, especially against respiratory and/or gastrointestinal diseases. NDV can be easily cultured to very high titers in embryonated eggs. Mass culture of embryonated eggs is relatively cheap. NDV vaccines are relatively stable and can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New avian paramyxovirus cDNA, useful for production of vaccine against Newcastle disease virus
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel avian-paramyxovirus cDNA (I) which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; lentogenic; F protein; vaccine;
gastrointestinal disease; poultry pathogen;
                                  DAA sequence of myotonic dystrophy gene - used to produce probes and identify CHR 19 abnormality and protein kinase responsible
                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                          Score 30; DB 14; Length 1093;
Pred. No. 5.5e+02;
L: Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprises a nucleic acid sequence corresponding to the 5'
                                                                                                                 The sequence is that encoded by predicted reading frame a the human myotonic dystrophy (DM) gene. It may be used in identification of individuals affected by DM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Newcastle disease virus LaSota genome encoded protein 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gielkens ALJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koch G,
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY51233 standard; Protein; 2204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 3; 115pp; English.
                                                                                      Disclosure; Fig 6; 64pp; English
                                                                                                                                                                                                                                              85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98EP-0202054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-NL00377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patients BPH, De Leeuw OS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-APR-2000 (first entry)
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Newcastle disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Avian-paramyxovirus;
respiratory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WFI; 2000-106102/09
WPI; 1993-288410/36
                                                                                                                                                                                            1093 AA;
                                                                                                                                                                                                                                                                                                                                     382 frprwr 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocal immunity.
                                                                                                                                                                                                                                                                                                               1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .7-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 - DEC - 1999
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XAY51233;
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                          AAY51233
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invention
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routes of infection of many other poultry pathogens. NDV can induce local immunity despite the presence of circulating maternal antibody. This sequence represents a protein encoded by the NDV strain LaSota genome which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antiqens, given in AAB53234 to AAB54006. The human colon cancer antiqens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment, and diagnosis of colon disorders, such as colon cancer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system disorders, muscular disorders, reproductive disorders, qastrointecstimal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC99764 to AAC99772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colon cancer associated gene sequences, referred to as colon cancer antiqens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
                                                                                                                                                                                                                                                                                                                                                                        Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; reproductive disorder; cardiovascular disorder; renal disorder; infectious disease; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polynucleoLides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune
                                                                                                                                        Gaps
                                                                                                                                        ;
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                                                                                                           Length 2204;
                                                                                                                                                                                                                                                                                                                                               Human colon cancer antigen protein sequence SEQ ID NO:1529.
                                                                                                                                      1; Indels
                                                                                                           Score 30; DB 21;
Pred. No. 1.1e+03;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 2083-2084; 2104pp; English.
                                                                                                                                                                                                                                                               AAB53989 standard; Protein; 90 AA.
                                                                                                          85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-2000; 2000WO-US05883
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                  Host Local Similarity 66.7
Matches 4: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-587534/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA, Ruben SM
                                                                    2204 AA;
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| 1844 frplwr 1849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                    09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000.
                                                                    Sequence
                                                                                                             Ouery Match
                                                                                                                                                                                                                                                                                          AAB53989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 [ii]. Length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Frimer sets for synthesizing polynucleotides, particularly the 5602 fuil-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harran; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                              Gaps
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                                                                                                     DB 21; Length 90;
                                                                                                                                                                          Indels
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Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota T. Isogai T., Nishikawa T., Hayashi K., S.
Ishii S., Sugiyama T., Wakamatsu A., Nagai K.,
                                                                                                                                                                      1; Mismatches
                                                                                                 Score 29; DB
Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human protein sequence SEQ ID NO:12886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS93531 standard; Protein; 217 AA.
                                                                                                 82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-2000; 2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUN-2001 (first entry)
                                                                                                                                                                          4; Conservative
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                                                                                                 Query Match
Best Local Similarity
90 AA;
                                                                                                                                                                                                                                                                                                             74 fkpcwk 79
                                                                                                                                                                                                                                        1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E91.074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C7 - FEB - 2001 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA:493531;
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AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
ប្តភ្ជព្ព័ន្ធ
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Sequence 217 AA;

Gaps 0; Ouery Match 82.9%; Score 29; DB 22; Length 217; Best Local Similarity 80.0%; Pred. No. 1.7e+02; Matches 4; Conservative 0; Mismatches 1; Indels

.; 0

1 FKPXW 5 ||||||| 164 fkpsw 168 ć

g G

Search completed: February 27, 2002, 11:41:16 Job time: 455 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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 protein search, using sw model OM protein February 27, 2002, 11:45:19; Search time 145.23 Seconds (without alignments) 3.147 Million cell updates/sec Run on:

US-09-446-109A-9 Title: Perfect score

1 PKPXWR 6 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* Database :

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		œ					•
Result No.	Score	Ouery Match	Length	DB	QJ	Description	u
				:			
-	33	94.3	380	~	C64364	formate hydrogenl	drogenly
7	33	94.3	412	7	E65146	hypothetical	sal 47.4
m	33	94.3	498	7	1171279	probable femA prot	emA prot
4	33	94.3	557	~	886020	hypothetical prote	sal prote
S	33	94.3	623	~	T18250	peptide transport	ansport
9	31	88.6		ď	S78199	probable	maturase
7	30	85.7		7	1172667	hypothetical	sal prote
æ	30	85.7		7	E65131	hypotherical	sal 47.5
6	30	85.7		~	B86002	probable amino aci	amino aci
10	30	85.7		~	н69805	conserved hypother	hypothet
11	30	85.7		7	T31640	. hypothetical	sal prote
12	30	85.7		~	S67568	probable membrane	nembrane
13	30	85.7	962	~	JC5808	G protein-coupled	-coupled
14	30	85.7		-	RRNZNV	genome polyprotein	lyprotein
15	29	82.9		~	T36433	hypothetical	sal prote
16	29	82.9		7	H64956	yedG protein	ein - Esc
17	29	82.9		~	F85810	hypothetical	_
18	29	82.9		7	T24993	hypothetical	sal prote
19	29	82.9	m	7	Н69147	LPS biosynthesis	thesis R
20	29	82.9		7	H75484	hypothetical	sal prote
21	29	82.9	435	2	C86340	protein F2D10.28	2D10.28 [
22	53	82.9		7	H82504	conserved hypothe	hypothet
23	56	82.9	162	~	T15052	amino acid	1 permeas
24	29	82.9	~	7	A59268	nodulation	n competi
	29	ć.	473	~	G72753	hypothetical	sal prote
56	58		477	~	877373	hypothetical	sal prote
27	29	82.9	488	7	B82967	probable glucose-6	11ncose-6
28 .	29	ς.	522	7	T05142	glutamatecystein	cystein
29	29	82.9	554	-	834607	carboxylesterase	sterasc (

Properby: ical 47.4 kD protein in rhsB-pit intergenic region - Escherichia coli (strain N.Al: schae names: hypothetical protein f409 C; Speries: Escherichia coli C; Data: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_cliange 08-Oct-1999 C; Accession: E65146; S47710 Biblather, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Kiley, M.; A.; R.Sse, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A; Title: The complete genome sequence of Escherichia coli K-12. A; Referênce number: A64720; MUID:97426617

A. Accession: E65146
A. Status: nucleic acid sequence not shown; translation not shown
A. Status: nucleic acid sequence not shown; translation not shown
A. Molecula type: DNA
A. Molecula: 1-412 CBLAT>
A. Cross: references: GB:AE000425; GB:U00096; NID:92367232; PIDN:AAC76515.1; PID:923672
A. Exo-srimental source: strain K-12, substrain MG1655
B. PLINESEL, G.
Submit:Gd to the EMBL Data Library, March 1994

asparagine synthas hypothetical prote pumilio family pro	C	hypothetical prote hypothetical prote	hypothetical prote hypothetical prote envelope protein E	transposase - Myco transposase - Flav	probable transloca chitinase (EC 3.2. hypothetical prote
T39308 T30044 T50143	S25952 T38755 T48944	S28301 D86400	T48945 B70438 VMWJBV	S10929 A49895	T37841 JE0183 E84788
777	000	77	~ ~ ~	77	777
557 655 732	1224 2685 84	162	195 227 233	254 254	273 275 297
32.9 82.9 82.9	82.9 82.9 30.0	80.0 80.0	80.0 80.0 0.0 0.0	80.0 80.0	80.0 80.0 80.0
53 53 73	29 28 28	28 28	7 7 8 8 8 7 8 7 8	28 28	28 28 28
30 31 32	ይህ ዚህ ሲና የህ ቀን ሲ	36 37	338 39.04	41 :	43 45 5

AL IGNMEN'FS

MESULT 1 C64364 C64364 C64364 C64364 C59ecies: Methanococcus jannaschii C50ecession: C64364 R58ult, C51; White, O.; Olsen, G51; Zhou, L5; Fleischmann, R.D.; Sutton, G.G.; Blak R58ult, C51; White, O.; Olsen, G51; Zhou, L5; Fleischmann, R.D.; Sutton, G.G.; Blak R58ult, C51; White, O.; Olsen, G51; Zhou, L5; Fleischmann, R.D.; Sutton, G64364 R58ult, C51; White, D64364 R58ult, C51; White, D64364 R64306, MUD196337999 R6406000000000000000000000000000000000
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Alternate names: gene cob intron 1 protein Chizosaccharomyces pombe) mitochondrion N.Alternate names: gene cob intron 1 protein C:Species: mitochondrion Schizosaccharomyces pombe C:Species: mitochondrion Schizosaccharomyces pombe C:Date: 29-Jan-1998 #sequence_revision 20-Feb-1998 #text_change 21-Jul-2000 C:Accession: S78199; S10070; S67378 R.Lang, B.F. Submitted to the EMBL Data Library, August 1990 A:Description: The mitochondrial genome of the fission yeast Schizosaccharomyces pombe and Aspergillus nidulans. A:Reference number: S78195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G. Superfamily: cytochrome b6 homology; cytochrome b homology; plastoquinol--plastocya C. Keywords: heme; iron; metalloprotein; mitochondrion F:1-228/Region: cytochrome b exon 1 encoded F:10-228/Jomain: cytochrome b homology #status atypical <CBII> F:10-228/Jomain: cytochrome b6 homology *CBE> F:10-228/Jomain: cytochrome b6 homology CBIO-210/Jomain: plastoquinol--plastocyanin reductase 17K protein homology #status a E;222-2:8/Jomain: cytochrome b intron encoded.
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State=1, B.G.: Rajandream, M.A.
Submitted to the EMBL Data Library, November 1998
A.Reference number: 218831
A.Accession: T18250
A.Status: pre-liminary; translated from GB/EMBL/DDBJ
A.Status: pre-liminary; translated from GB/EMBL/DDBJ
A.Molecuje type: DNA
A.Residues: 1-623 <BAR>
A.Cross references: EMBL:AL033503; NID:e1341066; PID:e1341077; PIDN:CAA22021.1
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                                                                                                                                                                                                                                                                                                      C.Species: Candida albicans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                               Gaps
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                               Indels
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                                                                                                                                                                                                                                                                               peptide transport protein - yeast (Candida albicans)
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Pred. No. 44;
0; Mismatches
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  Pred. No. 40;
0; Mismatches
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A;Accession: S10070
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A:Residues: 1-1035 <LAN>
A:Cross-references: EMBL:X54421
A:Experimental source: Strain ad7-50h
R:Lang, B.F.; Ahne, F.; Bonen, L.
J. Mol. Biol. 184, 353-366, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.3%;
  83.3%;
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A):Residues: 1-1035 <LAW>
A):Cross-references: EMBL:X02819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.3
Best Local Similarity 83.3
Matches 5; Conservative
                               5; Conservative
Best Local Similarity
Matches 5; Conserv
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A;Genetic code: SGC2
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445 FKPIWR 450
                                                                                                                   1 FKPXWR 6
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A;Introns: 475/3
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S78199
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C: Date: 16 Feb-2001 #sequence_revision 16 Feb-2001 #text_change 31 Mar-2001
C: Accession B66020
C: Accession B66020
Iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A: Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A: Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RiFraser, C.M.; Nořrls, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
Rson, J.; Khalak, H.; Richlardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc
they, L.; Weldman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
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A:Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Residues: 1-498 <COL>
A:Cross-references: CB:AE001251; CH:AE000520; NID:g3323111; PIDN:AAC65773.1; PID:g332311 A:Experimental source: strain Nichols A:Genetics: A:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770
A:Accession: H71279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable femA protein - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul.1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
                            A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-398, 'MLLSRCFAGS1' <PLU>
A:Cross-references: EMBL:U00039; NID:g466582; PIDN:AAB18466.1; PID:g466627
A:Rote: this sequence has been corrected
C:Genetics:
A:Gene: yhlL
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Pred. No. 30;
0; Mismatches
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0; Mismatches
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83.3%; Pred. No.
                                                                                                                                                                                                                                                                                                94.3%;
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Best Local Similarity 83.3
Matches 5: Conservative
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Matches 5; Conservative
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A;Molecule type: DNA
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240 FKPKWR 245
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                       A; Accession: S47710
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Kinnst F.; Ogasavara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, D.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabrel, C.; Ferrari, A.; Lindito, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabrel, C.; Ferrari, A.; Luci, ad., 29-256, 1997
A.Authora; G.; Rothyer, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J., Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.; Moetter, P.; Koningstein, G.; Krodh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino, A.; Authora; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau, Y. M.; Oqawa, K., Oqiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, G.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlesch, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiya A.; William, Y.; Vata, K.; Vata, K.; Voshida A.; Tit...: The Complete genome sequence of the Gram-positive bacterium Bacillus subtill A.; Reference number: A69580; MUID:98044033
probable amino acid/amine transport protein yhfm {imported} - Escherichia coli (strai C.Species: Escherichia coli C.Species: Escherichia coli C.Species: Escherichia coli C.Species: I6-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C.Species: B86002 B.Species: N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iler, G.; Grotbesk, E.J.; Davis, N.W.; Lim, A.; Dimalanta; E.; Potamousis, K.; Apoda Mature 309, 529-533, 2001 A.; Miller, Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                   A:Status: preliminary
A:Molecole type: DNA
A:Residues: 1-462 <STO>
A:Cross-references: GB:AE005174; NID:g12517998; PIDN:AAG58478.1; GSPUB:GN00145; UWGP:
A:Experimental source: strain 0157:H7, substrain EDL933
C:Genetics:
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A:Cross-references: GB:299108; GB:AL009126; NID:92633055; PIDN:CAB12672.1; PID:e11828
A:Expartmental source: strain 168
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C:Date. 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: B69805
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Pred. No. 1.7e+02;
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Pred. No. 1.3e+02;
1; Mismatches 1;
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66.78;
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Best Tocal Similarity
At Conserva
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Matches 4; Conserv
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398 YKPLWR 403
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C;Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTM10
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A:Experimental source: strain K-12, substrain MG1655
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E56131
hypothetical 47.5 kD protein in cysG-trpS intergenic region - Escherichia coli (strain in Species: Escherichia coli
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Space: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 17-mar-2000
C.Accession: E65131
R.Blattiner, R.R.: Plunkett III, G.; Bloch, C.A.: Perna, N.T.: Burland, V.: Riley, M.; C.A.: Rose, D.J.: Mau, B.; Shao, Y.
A. Rose, D.J.: Mau, B.; Shao, Y.
A.A. Rose, D.J.: Mau, B.; Shao, Y.
A. Reference number: A64720; MUID:97426617
A. Reference number: A64720; MUID:97426617
A. Status: preliminary; nucleic acid sequence not shown; translation not shown
A. Molecule type: DNA
A. Residuals: 1-462 vBLATA
A. Re
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                    Length 1035;
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Pred. No. 1.3e+02;
1; Mismatches 1; Indels
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                                                                                        1; Indels
                    Score 31; DB 2; 1
Pred. No. 1.8e+02;
1; Mismatches 1;
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Pred. No. 70;
1; Mismatches
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66.7%;
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Best Local Similarity 66.7%;
Matches 4; Conservative
                    88.6%;
66.7%;
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A,Gene: yhiM
C,Superfamily: arginine permease
                 Query Match 88.6
Bost Local Similarity 66.7
Matches 4; Conservative
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Bost Local Similarity
Matches 4; Conserv
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398 YKPLWR 403
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genome polyprotein - Newcastle disease virus (strain Beaudette C)
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: Newcastle disease virus
C;Date: 31-Mar-1969 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
C;Accession: A2647
R;Yusoff, K.; Miliar, N.S.; Chambers, P.; Emmerson, P.T.
M:Clock Rock Res: 15, 3961-3976, 1987
A:Title: Nucleotide sequence analysis of the L gene of Newcastle disease virus; homol A:Reference number: A3665; MUID:87230982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R)Seeger, K.: Harris, D.: James, K.D.: Parkhill, J.: Barrell, B.G.: Rajandream, M.A. submitted to the EMBL Data Library, July 1999
A;Reference number: 221598
A;Accession: T96433
A;Stacus: preliminary: translated from GB/EMBL/DDBJ
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A;Experimental source: strain A3(2)
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A;Residues: 1-2204 <YUS>
A;Cross-references: GB:X05399; NID:960937; PIUN:CAA28985.1; PIU:960939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: parainfluenza virus RNA-directed RNA polymerase C;Reywords: ATP; nucleotidyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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llarity 66.7%; Pred. No. 2.6e+02;
Conservative 1; Mismatches 1;
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                               A;Status: nucleic acid sequence not shown
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Best Focal Similarity 60...
Hestine 4; Conservative
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A; Residues: 1-119 <SEE>
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Best Local Similarity
Matches 4; Conserv
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1344 FRPLWR 1849
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A:Cross-references: EMBL:274083; NID:g1431014; PID:e252988; PID:g1431015; GSPDB:GNU0004;
A:Experimental source: strain S288C
                                                                                                                                                                                               A;MOLecule type: DNA
A;Residues: 1-684 <WIL>
A;Cross-references: EMBL:AL117195; NID:e1549729; PIDN:CAB55023.1; CESP:Y57A10A.r
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JC5808
G protein-coupled receptor I - yeast (Saccharomyces cerevisiae)
G protein-coupled receptor I - yeast (Saccharomyces cerevisiae)
C:Specios: Saccharomyces cerevisiae
C:Date: 04-Peb-1998 #sequence_revision 13-Mar-1998 #text_change 19-May-2000
C:Accession: JC5808
R:Vun, C.W.: Temaki, H.: Nakayama, R.: Yamamoto, K.: Kumagai, H.
Hiochem. Biophys. Mcs. Commun. 240, 287-292, 1997
A:Title: G-protein coupled receptor from yeast Saccharomyces cerevisiae.
A:Reference number: JC5808: MUID:98049822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable membrane protein YDL035c - yeast (Saccharomyces cerevisiae)
N.Alternale names: hypothetical protein D2749
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 29-Oct-1999
C:Accession: $67568
R:Paulin, b.: Saren, A.M.: Laamanen, 10.
submitted to the Protein Sequence Database, July 1996
A:Reference number: $67560
A:Reference number: $67560
C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Accession: T31640
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Pred. No. 1.9e+02;
1; Mismatches 1; Indels
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C:Keywords: transmembrane #status predicted <TMI>
F:57-104/Domain: transmembrane #status predicted <TM2>
F:140-156/Domain: transmembrane #status predicted <TM3>
F:181-197/Domain: transmembrane #status predicted <TM3>
F:256-272/Domain: transmembrane #status predicted <TM4>
F:623-639/Domain: transmembrane #status predicted <TM5>
F:662-678/Domain: transmembrane #status predicted <TM5>
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                                                                R.Smyc, R. Smyc, R. Smyc, R. Smyc, R. Smyc, R. Smyc, R. Submitted to the EMBL Data Library, September 1999 A. Reference number: 221048 A. Accession: 713140 A. Status: preliminary: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                        A: Experimental source: clone Y57A10A C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%;
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66.7%;
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Matches 4; Conserv
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Ouery Match 82.9%; Score 29; DB 2; Length 119; Best Local Similarity 66.7%; Pred. No. 57; Matches 4; Conservative 1; Mismatches 1; Indels

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Search completed: February 27, 2002, 11:45:19 Job time: 698:sec

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94.3%; Score 33;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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HS47_MOUSE
HS47_RAT
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CSAR_HUMAN
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DXR_BACSU
HS47_CHICK
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YM91_SCHPO
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                    Q9xyd3 caenorhabdl
Q95050 telrahymena
P03356 akv murine
Q50864 myxococcus
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caenorhabdi
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                                                                              potato leaf
                                                   mycobacteri
                                                                                                      akr murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | [:]
SEQUENCE FROM N.A.
SEQUENCE PROM N.A.
SERAINS-84316500: PubMed-8041620;
SOCIA H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
Socia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia cooli genome. V. DNA sequence of the
region from 76.0 to 81.5 minutes ";
".i.n. Acids Res. 22:2576-2586(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-ELLY MG1655;
MEDLINE-97426517; PubMed=9278503;
MEDLINE-97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V., R.Lipy M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Steavor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mai B., Shan Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Bacteria: Proteobacteria: gamma subdivision; Enterobacteriaceae;
Escherichia.
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P03357
083728
P55465
023051
                                             Q9cb81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YHIL_ECOLI STANDARD; PRT; 535 AA.
P37629; P37628;
01-ocr-1994 (Rel. 30, Created)
20-AGG-2001 (Rel. 40, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 61 6 KDA PROTEIN IN RHSB-PIT INFERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coll K-12.";
Science 277:1453-1474(1997).
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Hypothetical protein; Complete proteome.
SEQUENCE 535 AA; 61576 MW; 0046CE539989FDF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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                                                                        V70K_PLRVI
PODK_TREPA
Y4GI_RHISN
Y5GO_CLOAB
HBLI_CAEEL
ATX9_TETTH
POL_MLVAV
RFBC_MYXXA
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                          YDF7_SCHPO
GLPK_MYCLE
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Length 535;

DB 1;

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Best Local Similarity
                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli
                                                                                   NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                                               707 FKPSWK 712
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                                                   Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 FKPXWR 6
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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          Gaps
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         Indels
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1601FD3AE21B80EB CRC64;
         :
                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PEPTIDE TRANSPORTER PTR2.
                                                                                623 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7
25;
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Pred. No. 25;
0; Mismatches
ed. No. 22;
Mismatches
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83.3%; Pred. No.
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                                                                                 PRT;
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MEDLINE-95291458; Pubmed-7773409;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69941 MW;
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ilarity 83.3%;
Conservative
        Conservative
                                                                                STANDARD;
                                                                                                                                        Candida albicans (Yeast)
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                 NCBI_TaxID-5476;
                                       168 FKPDWR 173
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445 FKP1WR 450
                       1 FKPXWR 6
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YM91_SCHPO
ID YM91_SCHPO
                                                                               PTR2_CANAL
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PTR2_CANAL
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                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-AD7-50, MEDLINE-86011547; PubMed-4046021; Jang B.F., Ahne F., Bonen L.; Tie mitochondrial genome of the fission yeast Schizosaccharomyces pombe. The cytochrome b gene has an intron closely related to the first two introns in the Saccharomyces cerevisiae coxl gene."; J. Mol. Biol. 184:353-366(1985).
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Pred. No. 78;
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                                                                                                                                                                                                             Enkaryota, Fungi, Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomycetaceae;
01.NOV.1988 (Rel. 09, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SCRIZOSACCHAROMYCES pombe (Fission yeast).
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Interpro: IPR000442; Intron_maturse2.
Interpro: IPR000477; RVTse.
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Hygothetical protein; Mitochondrion
SEGUENCE 807 AA: 91637 MW; AFD7(
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large non-coding
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01-JUL-1989 (Rel. 11, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA POLYMERASE BETA SUBUNIT (EC 2.7.7.48) (LANGE STRUCTURAL PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
             MEDLINE-97426617: PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; mayhew geduence of Escherichia coli K-12.";
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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Yusoff K., Millar N.S., Chambers P., Emmerson P.T.;
"Nucleotide sequence analysis of the 6 gene of Newcastle disease
virus: homologies with Sendai and vesicular stomatitis viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00324; aa_permeases; 1.
Hypothetical protein: Transport; Transmembrane; Inner membrane;
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                                                                                                                                                                                      -! - SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 445;
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Paramyxoviridae; Paramyxovirinae; Rubulavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B98DF5944A5E1FEF CRC64;
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Pred. No. 71;
1; Mismatches
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EMBL; AE000413; AAC76395.1; ALT_INIT.
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Best Local Similarity
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445 AA;
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381 YKPLWR 386
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P11205:
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                                                                                                                                                                                                                                 This SWISS-PRJT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Gutstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an cmail to license@isb-sib.ch).
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Gaps
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MEDLINE-97426617; Pubmed-9278503;
Blockner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Kiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Resident, Kihara M., Kawagishi I., Macnab R.M.; "Dyganization of the Escherichia coli and Salmonella typhimurium chromosomes between flagellar regions IIIa and IIIb, including a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
03-NAG-2001 (Rel. 40, Last annotation update)
HERNTHEDICAL 24.5 KDA PROTEIN IN AMYA-FLIE INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.7%; Score 30; DB 1; Length 2204; 66.7%; Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "171:e complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CiterPro, 1PR001016; Paramyx_RNA_pol.
Pram; PF00946; Paramyx_RNA_pol; 1.
Prans Ferase; RNA-directed RNA polymerase.
SEQUENCE 2.204 AA: 248822 MW: C6788674D904802C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qe non-coding region.";
Cen. Microbiol. 139:1401-1407(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MERCLINE-93381452; PubMed-8371104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! SIMILARITY: TO YEAST YMR114C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X05399; CAA28985.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 277:1453-1474(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A26747; RRN2NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Nall. Acad. Sci. U.S.A. 93:15086-15091(1996).
-i- FUNCTION: SYNTHESIZES SELENOPHOSPHATE FROM SELENIDE AND ATP.
-i- CATALYTIC ACTIVITY: ATP + SELENIDE + H(2)O = AMP + SELENOPHOSPHATE
                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ziotnik A.;
"Identification of a novel selD homolog from eukaryotes, bacteria,
and archaea: is there an autoregulatory mechanism in selenocysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
SELENIDE, WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE (SELENIUM DONOR PROTEIN 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENCODED BY THE OPAL CODON, UGA.
SIMILARITY: BELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guimaraes M.J., Peterson D., Vicari A., Cocks B.G., Copeland N.G., Gilbert D.J., Jenkins N.A., Ferrick D.A., Kastelein R., Bazan J.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guimaraes M.J., Hazan J.F., Zlotnik A., Wiles M.V., Grimaldi J.C., Lee F., McClanahan T.:
An new approach to the Study of haematopoietic development in the yolk sac and embryoid bodies.":
Development 121:3335-3346(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE ACTIVE-SITE SELENOCYSTEINE IS
                                                                                                                                                                                                                               .
0
                                                                              Pfam; PF02286; DUF159: 1.
Hypothetical protein; Complete protecomc.
CONFLICT 213 217 TRARS -> NQGAELIQPV (IN REF. 1).
SEQUENCE 217 AA: 24500 MW; 4F26C95DB3B02900 CRC64;
                                                                                                                                                                                             Length 217;
                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ptam; PF00386; Alks; I.
Transferase: Selenium; Selenocysteine; ATP-binding.
                                                                                                                                                                                           DB 1;
57;
                                                                                                                                                                                                                                                                                                                                                                                      452 AA
                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                           Score 29;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
              EMBL: 1.13279; -; NOT_ANNOTATEL_CDS.
EMBL: AE000285; AAC74998.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:108388; Sps2.
InterPro; IPR000728; AIRS_related.
Pfam; PF00586; AIŖS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=96017645; Pubmed=7588067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-97140286; Pubmed-8986768;
                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - COFACTOR: SELENOCYSTEINE.
                                                                                                                                                                                         82.98;
66.78;
                                               EcoGene; EG13278; yedK.
InterPro; IPR003738; DUF159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U43285; AAC53024.1; -.
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASS I SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                    Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:108388;
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                                                                                                                                                                                                                                                                                           87 FKPLWQ 92
                                                                                                                                                                                                                                                            1 FKPXWR 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metabolism?";
                                                                                                                                                                                                                                                                                                                                                                                 SPS2_MOUSE
P97364;
                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                RESULT 7
SPS2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97061201: PubMed=8905231:
MEDLINE=97061201: PubMed=8905231:
Mayoluna N. Sato S. Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
Samura M., Yasuda M., Tabata S.;
"Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
DNA Res. 3:109-136(1996).
II. SIMILARITY: BELONGS TO THE UPF0061 FAMILY.
                             IMPORTANT FOR CATALYTIC ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
O
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                                                                                                                                                 Length 452;
                                                                                                                                              Score 29; DB 1; Length 452
Pred. No. 1.1e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Incerpro: TPR003846; UPP0061.
Pfam: PF02696; UPF0061; 1
Hypothetical protein: Complete proteome.
SEQUENCE 477 AA; 54041 MW; 81F6899B1A6D613C CRC64;
                                                                                                     9DA6F7250CFE80E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 54.0 KDA PROTEIN SLL1464.
                                              SIMILARITY).
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                           477 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             514 AA.
 POTENT IAL
                                                                      POLY - ALA.
                                                                                       POLY - ALA
                                                                                                                                                                                                                                                                                                                                                                                                                (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                   47786 MW;
                                                                                                                                             82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.98;
66.78;
                                                                                                                            Query Match
Best Mocal Similarity 66./",
".... 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                   452 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Symechocystis sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1148;
                                                        322
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433
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388 FSPSWR 393
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023736; Q43389;
                                                                                                                                                                                                                                   48 FSPSWR 53
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                                                                                                                                                                                                       1 FKPXWR
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                                                                                                                                                                                                                                                                                                           YZ64_SYNY3
P73436;
ACT_SITE
SE_CYS
SITE
                                                                                                     SEQUENCE
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                                                       UP_BIND
                                                                      DOMA IN
                                                                                                                                                                                                                                                                               RESUL: 8
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eudicots; Rosidae;

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CLUTAMATE - CYSTEINE LIGASE, CHLOROPLAST PRECURSOR (EC 6.3.2.2) (GAMMA-
                                         Arabidopsis thallana (Mouse-ear cress).
Ediarrycha: Virdalplantae; Streptophyta: Embryophyta: Tracheophyta: Sprimatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidomosiacophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidomosia II - frassicales; Brassicaceae; Arabidopsis.
              GLUTAMYLCYSFEINE SYNTHETASE) (GAMMA-ECS) (GCS). GSEL OR AT4G23100 OR F7H19.290.
                                                                                                                            SEQUENCE FROM N.A.
STATAIN-CO. COLUMBTA, TISSUE-Leaf,
MEDLINE-95023984; Pubmed-7937837;
MAY M.J., Leaver C.J.;
                                                                                                 NCHI_TaxID=3702;
                                                                                                                                                                                                                 homologs.
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  15-DKC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DGC-1998 (Rel. 40, Last annotation update)
GLUTAMATE--CYSTEINE LIGASE, CHLOROPLAST PRECURSOR (EC 6.3.2.2) (GAMMA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
MISCELLANGOUS: IN PLANTS, THERE ARE TWO FORMS OF THIS ENZYME, ONE
CYTOSOLIC AND THE OTHER CHLOROPLASTIC.
                                                                                                                                                                                                              Schaefer H.J., Hadg-Kerwer A., Rausch T.; cond cloning and expression analysis of genes encoding GSH synthesis in roots of the heavy-metal accumulator Brassica juncea L.: evidence for Cd-induction of a putative mitochondrial gamma-glutamylcysteine synthetase isoform.;
                                                                                                                                                                                                                                                                                                                                STRAIN-CV. VITTASSO; TISSUE-Leaf;
MEDLINE-9727256: Pubmed-9119067;
Schaefer H.J., Greiner S., Rausch T., Haag-Kerwer A.;
In seedlings of the heavy metal accumulator Brassica juncea, Cu2+
differentially affects transcript amounts for gamma-glutamylcysteine
synthetase (gamma-ECS) and metallothioneln (MT2)...
FEBS Lett. 404.216.220(1997).
                                                                                                  Eukaryota, Viridipiantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae;
eurosids II: Brassicales, Brassicaceae, Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORTHOPHOSPHATE + CAMMA-1.-GLUTAMYL-1.-CYSTEINE.
PATHWAY: FIRST AND RATE-LIMITING STEP IN DE NOVO GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glutathione biosynthesis, Ligase: Chloroplast: Transit peptide.
TRANSIT 1 55 CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . . . . . . . . . . . . . . . . . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 29; DB 1; Length or Pred: No. 1.38+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLUTAMATE - - CYSTEINE LIGASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07C71CB13E785FA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ( -> R (IN REF. 2).
-> I (IN REF. 2).
-> T (IN REF. 2).
                                                           GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS).
                                                                                        Brassica juncea (Leaf mustard) (Indian mustard)
                                                                                                                                                                                                       MEDLINE-98281577; Pubmed-9620267;
                                                                                                                                                                                                                                                                                        Plant Mol. Biol. 37:87-97(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57903 MW;
                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 126-342 FROM N.A.
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                                                                                                                                                                                                                                                                            synthetase isoform
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIOSYNTHESIS
                                                                                                                                            NCBI_TaxID=3707;
                                                                                                                                                                                         TISSUE-ROOT
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CONFLICT
SEQUENCE
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PROJUGNEE FORD N.A.

RYALINE-20083488; PubMed-10617198;

RMPDIANE-20083488; PubMed-10617198;

RMPDIANE-20083488; PubMed-10617198;

RMPDIANE-20083488; PubMed-10617198;

RA MASSEGRATION N. Stlekma W., Entian K.-D., Terryn N., Ratchester M., Gelineller C., Wamburt R., Watson M., Schmidthein T., Matchester D., Machael D., Matson M., Schmidthein T., Matchester D., Motelsel J., Zimmermann W., Watler H., Ridley P., Rays D., Motelsel J., Zimmermann M., Watler B., Dortetelle D., Perez-Alonso M., Boutry M., Bancroft I., RA VDS P., Motelsel J., Zimmermann W., Wadler H., Ridley P., RA Vos P., Motelsel J., Zimmermann W., Wadler H., Ridley P., RA Vos P., Motelsel J., Zimmermann W., Wadler H., Ridley P., RA Vos P., Motelsel J., Zimmermann W., Wadler H., Ridley P., RA Vos P., Motelsel J., Zimmermann W., Hilbert H., Braun M., Allier E., Brandt A., Peters S., Van Sastiaens I., Aert R., Defoor E., RA Wattzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Habert H., Braun M., Habert H., Motelsel J., Roeter P., RA Wattzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., And Montagu M., Rogers J., Cronin A., Quanderth S., Van den Daele H., Reflect A., Rajandream M.-A., Lyne M., Lennard N., Motaly K., Mayes R., Marsen A.C., Schaeler M., Muenler-Auer S., RA Gabel C., Puchs M., Partmann B., Granderath R., Dauner D., Herzl A., Scharle M., Scharle M., Cham M., Razvenet O., Quigley F., Clabad M., Bargues M., Terol J., Trores A., Schabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., Ray M., Lecharny A., Aubourg S., Ray M., Lechar S., Peter S., Peter S., Haber R., Rayser C., Monfort A., Caber S., Peter S., Peter S., Ray M., Lecharny A., Aubourg S., Ray M., Lechar S., Peter S.,
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*Arabidopsis thaliana gamma-glutamylcysteine synthetase is
structurally unrelated to mammalian, yeast, and Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cobbett C.S., May M.J., Howden R., Rolls B.;
"The glutathlone-deficient, cadmium-sensitive mutant, cad2-1, of
Aracidopsis thaliana is deficient in gamma-glutamylcysteine
                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. LANDSBERG ERECTA; STRAIN-CV. LANDSBERG ERECTA; Ullmann P., Gondet L., Bach T.J.; Ullmann P., Gondet L., Bach T.J.; all solution of an Aribidopsis thaliana cDNA encoding a putative gamma-glutamylcysteine synthetase by complementation of a GSHI deficient yeast mutant-glutamylcysteine synthetase."; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Silimitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 91:10059-10063(1994)
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STRAIN-CV. COLUMBIA;
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1; Mismatches

4; Conservative

Matches

204 FOPKWR 209

1 FKPXWR 6

Last annotation update)

Last sequence update)

(Rel. 32, Created) (Rel. 40, Last sequ (Rel. 40, Last anno

GSHI_ARATH STANDARD: P46309; 082759; P92951; OI.NOV-11995 (RRI. 32, Cre 20-AUG-2001 (RRI. 40, Las 20-AUG-2001 (RRI. 40, Las

GSH1_ARATH
ID GSH1_A
AC P46309
DT 01-NOV
INT 20-AUG
UT 20-AUG

RESULT 10

522 AA.

STANDARD;

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MEDLINE-93326638; Pubmed-7916639;
Aida K., Moore R., Negishi M.;
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                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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VRTGVTPAEKLLEMYNGEWGQSVDPVFEELLY -> GQNRS
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01-NOV-1997 (Rel. 35, Last Sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
LIVER CARHOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ES-MALE) (ESTERASE-31).
                                                                                                                                                                           -:- SUBCHLIALIAR LOCATION: CHLOROPLAST (PROBABLE).
-:- SUBCELLIAR LOCATION: CHLOROPLAST (PROBABLE).
-:- TISSUE SPECIFICITY: ABUNDANT IN LEAVES AND ROOTS.
-:- MISCELLANEOUS: IN PLANTS, THERE ARE TWO FORMS OF THIS ENZYME, ONE CYTOSOLIC AND THE OTHER CHLOROPLASTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caps
Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Antonoiu B., Zidanic M., Jones K., Drone K., Cotton M., Joshu C., Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnossy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M., Matlenssen R., McComble W.R., Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                      -1 - PATHWAY: FIRST AND RATE-LIMITING STEP IN DE NOVO GLUTATHIONE
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                                                                                                         Nature 402:769-777(1999).
-!- CATALYTIC ACTFOTITY: ATP + I.-CLUTAMATE + I.-CYSTEINE = ADP
ORTHOPHOSPHATE + GAMMA-L-GLUTAMYL-L-CYSTEINE
-!- ENZYME:-REGULATION: FEEDDACK INHIBITION DY GLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 29: DB 1; Length 522
Pred. No. 1.3e+02;
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STRAIN-BALB/CJ X DBA/2J; TISSUE-LIVEr;
                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.9%;
66.7%;
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Best Local Similarity
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                                                                                                                                                                     BIOSYNTHESIS
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212 FQPKWR 217
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Q63880;
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                                                                                               thaliana
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "!" SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
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PREVENT SECRETION FROM ER (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: MICROSOMAL MEMBRANE, LUMEN OF ENDOPLASMIC
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Bradyrhizobium group; Bradyrhizobium.
                                                                                            carboxylesterase in mouse liver.";
Blochim. Blophys. Acta 1174:72-74 (1993).
-!- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND THE ACTIVATION OF ESTER AND AMIDE PRODRUGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Narberhaus F., Weiglhofer W., Fischer H.M., Hennecke H.;
"Identification of the Bradyrhizobium japonicum degP gene as para: operon containing small hear shock protein genes.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
:- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
                                                                                                                                                                                                                                                                     -1- CATALYTIC ACTIVITY: A CARBOXYLIC ESTER + H(2)0 - AN ALCOHOL + A CARBOXYLIC ANION.
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O
Alda K., Moore R., Negishi M.; "Cloning and nucleotide sequence of a novel, male-predominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 554;
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Pred. No. 1.3e+02;
0; Mismatches 1;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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InterPro; IPR00379; Est_lip_thioest_actsite.
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SMALL HEAT SHOCK PROTEIN HSPD.
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80.0%;
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ACT_SITE
DISULFID
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CARBOHYD
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SEQUENCE
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SEQUENCE FROM N.A.
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                                                                                                                            Y1,56_CAEEL
Q03598;
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1D CGCC, H
AC 10-MAY
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                                                                                                                                                                  This SWISS-PKOT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muenchbach M., Nocker A., Narberhaus F.;
"Occurrence of a superfamily of small heat shock proteins in
Bradyrhizobium japonicum and other Rhizobium species: a plant-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
NCBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (AUG-1998) to the EMBI/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 28; DB 1; Length 151; 66.7%; Pred. No. 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heat shock; Multigene family.
SEQUENCE 151 AA; 17098 MW; DFE9809310AF6A28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FB44EF94FB599EE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                        EMBL, AJ003064; CAA05835.1; -
InterPro: IRR002068; Crystallin_HSP20.
Idam; PF00011; HSP20; 1
PROSITE: PS01031; HSP20; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ010144; CAA09014.1; -. InterPro; IPR002068; Crystallin_HSP20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMALL HEAT SHOCK PROTEIN HSPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat shock, Multigene family.
SEQUENCE 151 AA; 17272 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00011; HSP20; 1.
PROSITE; PS01031; HSP20; 1.
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Best Local Similarity 66.79
Three 4; Consurvative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 66.7
Matches 4; Conservative
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FSPLWR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | | ||
6 FSPLWR 11
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086110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson R., Angrough R., Anderson K., Baynes C., Berks M., Howfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dear S., Du Z., Durbin K., Favello A., Fraser A., Johnston L., Gardner A., Green P., Hawkins T., Hillier I., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopera A., Saunders D., Shownkeen R. Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Wargerson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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                                                                                                                                                                                                                                                                      Eukaryota; Matazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wonldman P.;
اال Mo of contiguous nucleotide sequence from chromosome III of C.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
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                                                                  01-FEB-1994 (Rel. 28, Created)
01-FSB-1994 (Rel. 28, Last sequence update)
30-RAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 18.5 KDA PROTEIN C40H1.6 IN CHROMOSOME 111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wormPep; C40H1.6; CE00114.
Hypothetical protein.
SEQUENCE 162 AA: 18537 MW; BDC03CE3BCE79D55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tu-MAY-2000 (Rcl. 39, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HYPOTHETICAL PROTEIN GGI-126.
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1.62 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed-7906398;
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STANDARD;
                                                                                                                                                                                                                                            Caenorhabditis elegans
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Matches 4, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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MEDIINE=20272150; PubMed=10810093;
Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
"Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.";
Genome Res. 10:703-713(2000).
-1- SIMIGARITY: STRONG, TO C.ELEGANS C40H1.6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF151884; AAD34121.1; -.
Hypothetical protein.
SEQUENCE. 167 Aa; 19458 MW; 1675D9187DC43E14 CRC64;
                             $\\ \text{$\frac{1}{2}} \\ \text{$\frac{1}{2}
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Search completed: February 27, 2002, 11:42:45 Job time: 544 sec

1 FKPXW 5 ||| | |21 FKPLW 125

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February 27, 2002, 11:50:09 ; Search time 281.76 Seconds (without alignments) 3.115 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                      473505 seqs, 146272329 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
2: sp_bacteria:*
3: sp_funq1:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc.*
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sp_unclassified:*
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.35
1 FKPXWR 6
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_virus:*
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                                                                                                                                                                 Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Q9eum2 corynebacte	Q57935 methanococc	083784 treponema p	Q9url7 candida alb	Q9xyp8 drosophila	Q9vy94 drosophila	Q9xj12 oryza sativ	Q9d3f2 mus musculu	Q9ye03 aeropyrum p	O9d9rl mus musculu	O31566 bacillus su	O52961 bacillus su	Q9na80 caenorhabdi	Q12361 saccharomyc	Q91jql arabidopsis	090341 newcastle d	Q9wmh6 newcastle d	Q9dLd3 newcastic d	Q9uvp2 emericella
SUMMARIES			ID	Q9EUM2	057935	083784	Q9URL7	Q9XYP8	090794	09xJ12	Q903F2	Q9YE03	Q9D9R1	031566	052961	09NA80	012361	091701	090341	91MM16	: 090LD3	09uvP2
			DB	. ~	-	~	٣	Ŋ	2	10	Ξ	-	11	~	7	S	٣	10	12	12	12	٣.
			Match Length DB	250	380	498	623	917	917	221	204	239	440	909	610	684	961	1232	2204	2204	2204	2454
		Query	tch	7.1	4.3	4.3	4.3	4.3	4.3	9.88	5.7	85.7	5.7	85.7	5.7	5.7	5.7	5.7	5.7	5.7	85.7	5.7
	æ	š	Ma	. 6	σ	σ	6	6	5	30	20	æ	æ	œ	æ	80	æ	æ	œ	œ	ဆ	80
			Score	34	33	33	33	33	33	31	30	30	30	30	30	30	30	30	30	30	30	30
		Result	CN	-	7	m	4	S	و	7	89	6	10	11	12	. 13	14	15	16	17	18	19

Oguv56 emericella Ogxaa5 streptomyce Ogzew4 klebsiella O6402 olasmodium	09cjp0 pasteurella 09njyl giardia lam 09n2y6 caenorhabdi 09f2r9 streptomyce	O9fs78 triticum ae O9nndz leishmania O33353 mycobacteri O22568 caenorhabdi		09c1b2 gibberella 094088 fusarium sp 09c1b9 fusarium sp 09kn89 vibrlo chol 040414 nicotiana s	
3 Q9UV56 2 Q9XAAS 2 Q9ZEW4 5 Q96402	20000	2020		mmm a 9	2000
2454 119 138 143	162 164 224 233	244 262 296 301	395 398 412 435 436	4447 4447 4458 458	467 473 488 557
85.7 82.9 82.9	882 922.9 922.9	88 8 8 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	882.9 82.9 82.9 82.9 85.0 85.0	882.9 822.9 822.9 822.9	82.9 82.9 82.9 9.0 9.0
30 730 730	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	29 29 29	2000000000000000000000000000000000000	50 50 50 50 50 50 50 50 50 50 50 50 50 5	50 50 50 50 50 50 50 50 50 50 50 50 50 5
20 21 22 22 23 23 23 23 23 23 23 23 23 23 23	2222 4635	8 8 8 8 8 8 9 9 9 8	. W W W W W	33 38 39 40 41	4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5

ALIGNMENTS

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Gaps
                                                                                                                                                                                                                                               "Rauch A., Puehler A., Kalinowski J.; "Cala sequence and genetic organization of the integron-carrying R-planaid pCG4 of Corynebacterium glutamicum."; "Grantted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
"SMRH: AF164956, AAG00294.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                                                                                                                                                                                                                                                 97.1%; Score 34; DB 2; Length 250; 83.3%; Pred. No. 35; 1: Indels iive 0; Mismatches 1: Indels
                                                                                                                    Corynebacterium glutamicum (Brevibacterium flavum).
Piasmid R-piasmid pCG4.
Backoria; Pirmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                             Actinomycetalis; Corynebacterineae; Corynebacteriaceae;
Cirynebacterium.
WFBI_TaxID+s/18;
                                                                                                                                                                                                                                                                                                                                                            SEMUTENCE 250 AA; 28804 MW; 195C86367B483157 CRC64;
                                                (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                         250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         380 AA.
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                  Procedure, IPR002145; CopG_HTH_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Quory Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                    SEGUENCE FROM N.A. SERAIN-ATCC31330;
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214 EKPAWR 219
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                                                  01. MAR-2001 (
01. MAR-2001 (
01. JUN-2001 (
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40 057±35;
                                      OBERTM2:
                        Q9EUM2
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357933
RESULT
           U9EUM2
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Candida albicans (Yeast).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 FKPIWR 450
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Barrell B.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 FKPXWR 6
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                                                                                                                                                                                spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q9URL7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- COFACTOR: NICKEL (BY SIMILARITY).
--- PATHWAY: HYDROGEN METABOLISM: FHI, PATHWAY (BY SIMILARITY).
--- SUBUNIT: FHL COMPRISES OF A FORMATE DEHYDROGENASE, UNIDENTIFIED ELECTRON CARRIERS OF A FURNOCENASE (ISOENZYME 3). IN THIS NON-ENERGY CONSERVING PATHWAY MOLECULAR HYDROGEN AND CARBODIOXIDE FROM FORMATE ARE RELEASED (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE COMPLEX I 49 KDA SUBUNIT FAMILY.
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMHLrel. 17, Last annotation update)
PUTATIVE FORMATE HYDROGENLYASE SUBUNIT 5 (FHL SUBUNIT 5) (HYDROGENASE-
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-9633799; PubMed-8688087;
MEDLINE-96337999; PubMed-8688087;
MEDLINE-96337999; PubMed-8688087;
MEDLINE-96337999; PubMed-8688087;
Buit C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Rerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reitch C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fulfmann J.L.,
Utterback T.R., Kelley J.M., Peterson J.F., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.P., Frascr C.M., Smith H.O., Woese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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BUDLINE-9833270: PubMcd-9665876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR00135; Complex1_49kd.
InterPro; IPR001501; NiFeSe_Hases.
InterPro; IPR00146; complex1_49kd; 1.
Pfam; PF00744; NiFeSe_Hases; 1.
PR051TE; PS00535; COMPLEX1_49k; UNKNOWN_1.
PROSITE; PS00507; NI_HGENASE_L_1; UNKNOWN_1.
Hypothetical protein; Oxidoreductase; NAD; Iron-sulfur; 4Fe-4S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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                                                                                                                                                                                                     Methanococcus jannaschil.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43638 MW; 3EAD16D67834A76F CRC64
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Last annotation update)
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08,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 273:1058-1073(1996)
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SEQUENCE 380 AA; 43638
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Best Local Similarity 83.3
Matches 5; Conservative
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083784;
01-NOV-1998 (TYEMBLYCL).
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                    NCB1_TaxID-2190;
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241 FKPVWR 246
                                                                                                                                       COMPONENT E)
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                                                                                                                                                                                                                                                                         Methanococcus
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Khalak H., Richardson D., Howell J.K., Chidambaram M., Ullerback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C., "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tait E., Simon M.C., King S., Brown A.J., Gow N.A.K., Shaw D.J.;
"A Candida albicans Genome Project: Cosmid Contigs, Physical Mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 1.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy L., Harris D.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrell B.G., Rajandream M.A.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01022; PTR2_1; 1.
PROSITE; PS01023; PTR2_2; UNKNOWN_1.
SEQUENCE 623 AA; 69943 MW; 8543A3B1F7E7363E CRC64;
                                                                                                                                                                                                                                                                                                         498 AA; 56074 MW; 81710E41264431B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61.MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 2;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       623 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fungal Genet. Biol. 21:308-314(1997).
EMBL; AL033503; CAA22021.1; -
InterPro; IPR000109; PTR2.
Ffam; PF00854; PTR2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STGAIN=1161;
MEDLINE=97435544; PubMed=9290243;
                                                                                                                                            Science 281:375-388(1998).
EMBL; AE001251; AAC65773.1; -.
TIGR; TP0806; -.
                                                                                                                                                                                                                                                                                                                                                                                   94.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.3%;
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Best Local Similarity 83.55,
has 5; Conservative
                                                                                                                                                                                                                            InterPro; IPR003447; FemAB.
Pfam; PF02388; FemAB; 1.
Complete proteome.
SEQUENCE 498 AA; 56074 M
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94.3%; Scor
83.3%; Prec
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Best Local Similarity
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203 FRPTWR
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MULINE-20196006; PubMed-10731132;

MEDLINE-20196006; PubMed-10731132;

Addams M.D. Celniker S.E., Holt N.A., Evans C.A., Gocayne J.D.,
Addams M.D. Celniker S.E., Holt N.A., Evans C.A., Gocayne J.D.,
A manatides P.G., Scherer S.E., Holt N., Hoskins R.A., Galle R.F.,
A George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Channpe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,
Beeson K.Y., Benos P.V., Derman B.P., Bhandari D., Bolshakov S.,
A Burtis K.C., Busam D.A., Buller H., Cafleu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Clodek A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN -2001 (TrEMBLrel. 17, Last annotation update)
01-JUN -2001 (TrEMBLrel. 17, Last annotation update)
01-JUN -2001 (TrEMBLR LAST -2007)
01-JUN -2007 (TremBlr LAST -2007)
0200 (TremBlr Melanogaster (Fruit fly)
0200 (TremBlr Melazoa) Arthropoda; Tracheata; Hexapoda; Insecta;
0200 (TremBlr Last -2007)
0200 (TremBlr Las
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Last annotation update)
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                                            91.7 AA
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
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                                                 P.K.T. ;
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Matches 5: Conservative
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                                                 PRELIMINARY;
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657 FKPLWR 662
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Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibbegwam C.,
Jaiali M., Kallush F., Karpen G.H., Ke Z., Kenniscu J.A., Ketchum K.A.,
Kallai M., Kallush F., Kadira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Laixo P., Lai Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
A. Merkalov G. Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Acison D.R., Nelson K.A., Nixon K., Nusskern D.R., Parle I.A.,
Acison D.R., Nelson K.A., Nixon K., Nusskern D.R., Parle I.A.,
Reinert K., Semington K.S., Pan S., Pollated J., Puri V., Reese M.G.,
Reinert K., Semington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Klamos I., Singson M., Skupski M.P., Smith T.,
Shue B.C., Siden Klamos I., Singson M., Skupski M.P., Smith T.,
Shue B.C., Siden Klamos I., Stapleton M., Strong R., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
K. Weilliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
K.A. Weinston S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
K.A. Weinston S.W., Wooderi J.S., Zhan M., Zhang G., Zhao Q., Zhao G.,
Shibb R.A., Myers E.W., Kubin G.M., Venter J.C.;
Science 287,2185-2195-219000).
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Bakaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bakaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Shriartoideae; Poaceae;
Oryzeae; Oryzeae; Oryza
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STRAINECV. MIPPONBARE:
SERAIT T., Nagamura Y., Yamamolo K.;
C-yza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC chome:P0680AJ3."
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66.7%: Pred. No. 1.2e+02;
Live 1; Mismatches 1; Indels
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EMBL. AB023482; BAA78741.1: -- SEGUENCE 221 AA; 24502 MW; DC24FF370660BC15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR000634; dehydrtse_ser_thr.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
SEQUENCE 917 AA; 103706 MW; 6AEE88C211D256BB CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-4IN-2000 (TrEMBLrel. 14, Last annotation update)
HYPCTHETICAL PROTEIN.
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EMBL: AP000060; BAA79744.1;
InterPro; IPR001454; Hydrolase.
InterPro; IPR000150; Hypothet_cof.
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                                                                                                                                                                                                                                                                                                                                                                   135 FKPSWQ 110
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SEQUENCE FROM N.A.

STRAIN-C57DL/6J; TISSUE-THYMUS;

KRAWAI J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa T., Yasha M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuehl P., Lewis S., Matsuo Y., Nikaido I., Resole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Mashio T.,

Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez L., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming C.,

Mynshaw-Boolis A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional annotation of a full-length mouse cDNA collection.";
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1. 17, Last sequence update)
1. 17, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 24.8 KDA PROTEIN APE0766.
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Pred. No. 1.7e+02;
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                      01-JUN-2001 (TrEMBLrel
01-JUN-2001 (TrEMBLrel
                                                                      5830420C20RIK PROTEIN
                                                                                                                           Mus musculus (Mouse)
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Best Local Similarity
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29 FRPRWR 34
                                                                                               5830420C20RIK.
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X Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Kawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Kawal J., Shinagawa A., Shibata K., Yoshino H., Adachi J., Fukuda S., Anrawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashurnor M., Batalov S., Casavant T., Fleischmann W., Gasterland T., Cissi C., King B., Kochwa H., Antible, L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Fuuro M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Browstein M.J., Bult C., Fletcher C., Fuljita M., Gariboldi M., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wishiaw-Barshi H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Whitming L., Washiawaki S., Kawaji H., Kohtsuki S., Wasashi J., Kawashi J., Kawashi J., Kawashi J., Kawashi J., Kawashi J., Kohtsuki S.,
                                                                                                                                                                                                                                                                          Gaps
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ADULT MALE TESTIS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,
CLONE:1700030N20, FULL INSERT SEQUENCE.
                                                                                                                                                                                                  Score 30; DB 1; Length 239, Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                   1; Indels
Pram; PF00702; Hydrolase; 1.
PROSITE; PS01229; COF_2; UNKNOWN_1.
Hypothetical protein: Complete proteome.
SEQUENCE 239 AA; 24758 MW; EA30A3CDFD86B3DE CRC64;
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MGD: MGI:1923275; 5830420C20Rik.
                                                                                                                                                                                                  85.78;
66.78;
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Best Focal Similarity
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Matches 4, Conserv
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MEDLINE-97101647; PubMed-8946165; Yamamoto H., Uchiyama S., Sekfguchi J.; "Clouing and sequencing of a 27.8-kb nucleotide sequence of the 79 dermes-81 degrees region of the Bacillus subtilis genome containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nemaloda; Chromadorea; Rhabdilida; Rhabdiloidea;
Rhabdilidae; Peloderinae; Caenorhabdilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.7%; Score 30; DB 5; Length 684
66.7%; Pred. No. 5.3e+02;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Investigating biology.";
Science 282:2012-2018(1998).
Embi: AL117195; CAB550231.; -
SEPISNCE 684 AA; 79659 MW; FOE4FAF28EAFF687 CRC64;
                                                                                                                                                                                                                                                                 EMBL; D85082; BAA24464.1; -.
SEQUENCE 610 AA; 69089 MW; 34094DD5CA72FF66 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
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HYPOTHETICAL 110.7 KDA PROTEIN YDL035C.
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01-NOV-1996 (TrembLrel. 01, Last seq
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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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Matches 4; Conserv
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                                                                                         SEQUENCE FROM N.A.
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                                                NC91_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             672 FKPKWK 677
                                                                                                                                                                                                                   the sspE locus
DNA Res. 3:257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 FKPXWR 6
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012361;
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Q9NA80
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င်
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Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
RA Brouillet S., Burschi C., Brans A., Braun M., Bignell S.C., Bron S.,
RA Brouillet S., Burschi C., Brans A., Braun M., Bignell S.C., Bron S.,
RA Brouillet S., Burschi C., Brans A., Brain M., Bignell S.C., Bron S.,
RA Brouillet S., Brington J., Fabret C., Ferrari E., Foulger D.,
RA Chils S.K., Codani J.J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haicel J., Harwood C.R., Henatt A.,
RA Guiseppi G., Guy B.J., Haga K., Haicel J., Harwood C.R., Henatt A.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haga K., Rienchard M., Klein C.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurla K., Levine A., Lardinols S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Mostl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Porterelle D., Porwollik S., Prescott A.M.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Schuchi A., Tacconi E., Takagi T., Tarkagi T., Tarkamaru K.,
RA Sorokin A., Tacconi E., Takagi T., Tarkaga H., Vassancuti A.,
RA Sorokin A., Tacconi E., Takagi T., Tarkaga H., Wambult R., Wanbult R., Wedler E., We
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.7%; Score 30; DB 2; Length 606
66.7%; Pred. No. 4.7e+02;
iive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 299108; CAB12672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              606 AA; 68677 MW; 4B58DD58922ED0CA CRC64;
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Last sequence update)
Last annotation update)
                                             Last sequence update)
Last annotation update)
                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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                            Created)
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                                                                                                                                                                                                                                                                                                                  MEDLINE=98044033; PubMed=9384377;
                    01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE 606 AA;
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                                                                                                                                            Bacillus subtilis.
                                                                                                                                                                                                                                                                      SEQUENCE: FROM N.A.
                                                                                                                                                                                                                        NCBI_TaxID-1423;
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570 YKPEWR 575
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                                                                                                 YFIX PROTEIN.
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Gaps

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052961; 052961 RESULT 12 052961

Matches

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Length 684;

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Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
Trd and Bac clones.";

ID DNA Res. 7:217-221(2000).

-1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

REMEL: APROG044; BAD01179.1;

RIMEL: APROG044; BAD01179.1;

RIMER: PROG144; ATPRASC_AIPHa_beta.

RILECTPO: IPROG044; ATPRASC_AIPHa_beta.

RILECTPO: IPROG044; ATPRASC_AIPHa_beta.

RILECTPO: IPROG044; ATPRASC_AIPHA_BETA: UNKNOWN_1.

RICCTPO: SMOOL 18 RING: 1.

RR SMART: SMOOL 18 RING: 1.

RR SMART: PSOOL 19: CYTOCHROME_C: UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Rosidae;
eurosids II; Brassicales: Brassicaceae: Arabidopsis.
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Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                      SEQUENCE FROM N.A.
STRARH-ALPHN S28AEA
FRUILIN L., Saren A.M.;
Submitted (APR-1996) to the EMBL/GenBank/UDBJ databases.
                                                                                                                                                                                                                                                                            D3770C4A90699207 CKC64;
                                                                                                                                                              Paulin L., Saren A.M., Laamanen P.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                     MIPS)
Submitted (JJL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GRIAAD55299.1.
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Pubmed-10907853;
NCBI_Tax1D=4932;
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Gaps

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1; Indels

Score 30; DB 10; Pred. No. 9.2e+02; 1; Mismatches 1;

Query Match
Hest Local Similarity 66.7%;
Matches 4; Conservative

Length 1232;

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Do 902 FKPGWK 907
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1 FKPXWR 6

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Search completed: February 27, 2002, 11:50:10 Job time: 989 sec

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THER INFORMATION:
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Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 351, App
Sequence 35, Appl
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Sequence 1, Appl 1
Sequence 2, Appl 1
Sequence 113, Appl 5
Sequence 113, Appl 5
Sequence 113, Appl 5
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Sequence 113, App
Sequence 113, App
Sequence 113, App
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Sequence 2, Appli
                                                                                                                                                                                                                                                       (without alignments)
1.021 Million cell updates/sec
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                                                                                                                                                                                                                     February 27, 2002, 11:36:04; Search time 132.19 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-829-110-3
US-08-118-270-35
PCT-US93-08528-35
US-08-458-970A-9
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US-08-876-874-2
US-08-906-769-113
US-08-906-616-113
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US-08-639-075A-113
US-09-012-431-113
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US-08-906-613-113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212252 seqs, 22503292 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM protein – protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum UB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
US-09-143-438-5	US-08-254-989-2	US-09-413-814-10	US-09-091-219-25	US-09-091-219-2	US-08-704-655-20	US-08-665-543B-4	US-08-766-858A-27	US-09-164-193-8	US-08-997-080-75	US-08-997-362-75	US-08-873-970-75	US-09-095-855-75	US-09-334-601-13	US-08-997-080-194	US-08-997-362-194	US-09-095-855-194	US-08-351-981-6	
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77.1	17.1	77.1	17.1	17.1	74.3	74.3	74.3	74.3	74.3	74.3	74.3	74.3	74.3	74.3	74.3	74.3	74.3	
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ALIGNMENTS

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/label= BH /note- "either the natural phenylalanine amino terminus or the Bolton-Hunter modified peptide

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OTHER INFORMATION: having the group 3-(p-hydroxypenyl)propionyl group

NAME/KEY: Modified-site

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SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE: C5aR(133-148)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: Peptide
; LOCATION: 1..16
US-08-079-051-2
                                                                                                                                                                                                                                              Los Angeles
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICA'FION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: li
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| FKPIW 11
                                                                                                                                                                                                                                                                                                ZIP: 90067
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                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                              ClrY: STATE:
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                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                   ...rulcanT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: Krieger, Timothy J.
APPLICANT: Taylor, Robert
APPLICANT: Erfle, Douglas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS USING ANALOGUES OF INDOLICIDIN NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BENTO.
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Pred. No. 8.3;
1; Mismatches 1; Indels
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                            Length 6;
LOCATION: 4
OTHER INFORMATION: /label- dCha
OTHER INFORMATION: /note- "D-cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURENT APPLICATION DATA: APPLICATION NUBBE: US/08/915,314 FILING DATE: 20-AUG-1997 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                         0; Mismatches
                                                                                                                     /note- "D-arginine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: No. 6180604 tenburg Ph.D., Carol
RECISTRATION UNDBER: 39,317
REFERENCE/DOCKET NUMBER: 660081.405
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                         94.3%; Score 33; 100.0%; Pred. No.
                                                                                                       /label- dArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                          ESULT 2
S-08-915-314-26
Sequence 26, Application US/08915314
Patent No. 6180604
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ 110 NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 13 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%;
66.7%;
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                                                                   NAME/KEY: Modified-site LOCATION: 6
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Best Local Similarity 60.00
Free 4: Conservative
                                                                                                                                                                                                                         Conservative
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                                                                                 LOCATION: 6
COTHER INFORMATION:
COTHER INFORMATION:
US-08-215-137-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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Gaps

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10;
Sequence 2, Application US/08079051
Patent No. 5480974
GENERAL INFORMATION:
APPLICANT: EMBER, JULIA A.
APPLICANT: HUGLI, TONY E.
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application PC/TUS9406994
GENESAL INFORMATION:
APPLICANT: The Scripps Research Institute
TITHE OF INVENTION: ANTIBODIES TO HUMAN C5a RECEPTOR
KNAMER OF SEQUENCES: 4
CORRESPONDENCES: 4
CORRESPONDENCES: ADDRESSEE: SPARSES: ADDRESSEE: SPARSES: STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/079,051 FILING DATE: 18-JUN-1993
                                                                                                                                                                                                                               ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2790
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%; Score 28;
80.0%; Pred. No.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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10-AUG-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-513-974B-351
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Patent No. 6114139

GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Fujii, Ryo
APPLICANT: Fujii, Ryo
APPLICANT: Fusuni, Shoji
APPLICANT: Fusuni, Shoji
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Optaki, Tetsuya
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION:
MIMMED OF CERTIFICATION, AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 5; Length 16; Pred, No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: DIKE, HRONSTEIN, KOBERTS & CUSHMAN, LLP
130 Water Street
                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US94/06994
FILING DATE: 20-JUN-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPL/CATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME:::Tumarkin, Lisa A.
REGISTRATION NUMBER: P-38,347
REERENGE/DOCKET NUMBER: FD-2790
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
                           MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%;
80.0%;
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Best Local Similarity 80.0.
                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: C5aR(133-148)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
PCT-US94-06994-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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FILING DATE: 10-MGG-1993

FULING DATE: 10-MGG-1993

FULING DATE: 10-MGG-1993

FULING DATE: 10-MGG-1993

FULING DATE: 10-MGG-1995

FULING DATE: 10-MGG-1995

FULING DATE: 20-MGG-1995

FULING DATE: 20-MGG-1994

FULING DATE: 20-MGG-1994

FULING DATE: 30-MGG-1994

FULING DATE: 30-MG
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Sequence 35, Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
(ITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF NUMBER OF SEQUENCES: 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TREE: Floppy disk
FILING DATE: Floppy disk
FLOPPY DATE: Floppy disk
FLOPPY D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 1;
Pred. No. 1.9e+02;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 5;
Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
TYREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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REFERENCE/DOCKET NUMBER: MURPHY=2A TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197 TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFRAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 248633
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.0%;
80.0%;
                                                                                                                                                                                                                                                                            LENGTH: 304 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 amino acids
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Best Jocal Similarity 80.0'
                                                                                                               TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
EENGTH: 304 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     : MOLECULE TYPE: peptide US-08-118-270-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: peptide PCT-US93-08528-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 FKPIW 107
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PCT-US93-08528-35
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Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,110
FILING DATE: Filed Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 2; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTOWNEY/AGENT INFORMATION:
NAME: TOWNSEND, KEVIN G.
REGISTRATION NUMBER: 34,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 243 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOCY: linear
IMMEDIATE: SOURCE:
LIBRARY: THYWNOTO2
CLONE: 343504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 80.0
Matches 4: Conservative
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                            94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || || || 71 || 11 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 || 75 
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TETLE OF INVENTION: THERAPEUTIC AND SCREENING TETLE OF INVENTION: METHODS USING C3A RECEPTOR AND C3A
                                                                                                                                                      SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; DB 3;
Pred. No. 2.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                        APPLICATION NUMBER: US/09/082,310
FILING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 99-0520 US
TELECOMMUNICATION INFORMATION:
                                                                                                 E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDICATION DATA: APPLICATION NUMBER: 60/019,627 PILING DATE: 16-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-876-874-2; Sequence 2, Application US/08876874; Pate::: No. 5942405 c. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CLTY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRI

7.P. 19482

CONPUTER READABLE FORM:

MEDIUM TYPE: Diskette

MEDIUM TYPE: IBM Compatible
                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFUTARATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ames, Robert
APPLICANT: Bergsma, Derk
APPLICANT: Foley, James
APPLICANT: Kumar, Chandrika
                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sarau, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 536
     CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSA
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: PA
                                         COUNTRY:
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APPLICANT: Lal, Proeti
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Yue, Henry
"ITLE OF INVENTION: HUMAN NUCLEIC ACID METHYLASES
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                            APPLICAWT: LI, ET AL.

"ITLE OF INVENTION: C5a Receptor
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART 6 OLSTEIN
STREET: 6 BECKER FANM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB 2; 1
Pred. No. 2.2e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/458,970A FILING DATE: June 2, 1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/US94/09234 FILING DATE: 16 AUG 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: WULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERNCE/DOCKET NUMBER: 325800-353
TELECOMMUNICATION IRPORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                         : Sequence 9, Application US/08458970A
: Patent No. 5861272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-082-310-1
: Sequence 1, Application US/09082310
: Patent No. 6096526
                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%;
80.0%;
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INFORMATION FOR SEQ 1D NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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; MOLECULE TYPE: protein
US-08-458-970A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Rest Local Similarity
                                                                                                                                              GENERAL INFORMATION:
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103 FKPIW 107
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ZIP: 07068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 FKPXW 5
                                                                                        US-08-458-970A-9
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APPLICANT:
               a
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Length 463; 1; Indels

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APPLICANT: Grieve, Robert B.
APPLICANT: Grieve, Robert B.
APPLICANT: Grieve, Robert B.
APPLICANT: Rushlow, Kelth E.
APPLICANT: Rushlow, Kelth E.
APPLICANT: Stiegler, Gary
APPLICANT: Stiegler, Gary
APPLICANT: Sliver, Gary
TITLE OF INVENTION: FLEA AMINOPEPTIDASE PROTEINS AND USES THEREOF
NUMBER OF SEQUENCES: 190
COPRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
                                                                                                                               .;
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                                                                                      Length 496;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,616
FILING DATE: 05 AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 28; DB 3; 1
80.0%; Pred. No. 3.1e+02;
                                                                                    Score 28; DB 3; Pred. No. 3.1e+02;
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                                                                                                                             0; Mismatches
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; Pateni No. 6139840
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              US-08-996-616-113
: Sequence 113, Application US/08906616
; Patent No. 6121035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
"AME: Connell, Gary J.
"EGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
"ELEPHONE: (303) 863-9700
"TELEFAX: (303) 863-0223
INFORMATION FOR SEO ID NO: 113:
SEDUENCE CHARACTERISTICS:
                                                                                    80.0%;
80.0%;
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Best Local Similarity 80.0
Matches 4; Conservative
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    / MOLECULE TYPE: protein US-08-9:)6-769-113
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                                                              Ouery Match
Best local Similarity
Thus 4; Conserve
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STATE: Colorado
COUNTRY: USA
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358 FKPKW 362
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US-08-8:7-795-113
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APPLICANT: Stiegler, Gary
APPLICANT: Glines, Patrick J.
APPLICANT: Gliver, Gary
TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
UNBER OF SEQUENCES:
ADDRESSEE: Sheridan Ross & MCIntosh
                                                                                                                                                                                                                                                                                                                                                                                Length 482;
                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPUTER:
COMPUTER: PLOPPY disk
COMPUTER: PC-105/MS-105
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
APPLICATION NUMBER: US/08/906,769
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                Score 28; DB 2;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: JA00 Lincoln Street, Suite 3500 CITY: Denver STATE: Colorado
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REGISTRATION NUMBER: 32,020
REFERENCE/JOCKET NUMBER: 2618-25-C2
TELECOMINICATION INFORMATION:
TELEPAX: (303) 863-9700
TELEFAX: (303) 863-023
INFORMATION FOR SEO II) NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 496 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/639,075
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 113, Application US/08906769
Patent No. 6077687
GENERAL INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: PRESTATA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: P505
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0701
TELEPHONE: 610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Grieve, Robert B. APPLICANT: Rushlow, Keith E. APPLICANT: Wu Hunter, Shirley
                                                                                                                                            TELEX: 846169
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                80.0%;
80.0%;
                                                                                                                                                                                                             LENGTH: 482 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                            Query Match 80.0
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                       single
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                                                                                                                                                                                                                                                  STRANDEDNESS: sir
TOPOLOGY: linear
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TOPOLOGY: linear
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CORRESPONDENCE ADDRESS:
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: Colorado
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358 FKPKW 362
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                              ADDRESSEE:
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                                                                               STATE: C
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                                                                                                         APPLICANT: Arfsten, Ann
APPLICANT: Dale, Beverly
APPLICANT: SLEGIEF, Gary
TITLE OF INVENTION: USE OF PROTEASE INHIBITORS AND
TITLE OF INVENTION: PROTEASE VACCINES TO PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: INFESTATION, AND FLEA PROTECT ANIMALS FROM FLEA
TITLE OF INVENTION: MOLECULES, AND USES THEREOF
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: FLEA PROTEASE PROTEINS, NUCLEIC ACID
TITLE OF INVENTION: MOLECULES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,795
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3.1e+02;
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1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14442
Grieve, Robert B.
Rushlow, Keith E.
Hunter, Shirley Wu
Frank, Glenn R.
Heath, Andrew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 113, Application US/08639075A Patent No. 6150125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Gary J. Connell
RECISTRATION NUMBER: 32,020
REFERENCE//DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 11BM PC COMPATIBLE
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Rushlow, Keith E.
Wu Hunter, Shirley
Frank, Glenn R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 113: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stiegler, Cary
Gaines, Patrick J.
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 496 amino acids
TYPE: amino acid
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-817-795-113
                                                                                                                                                                                                                                                                                                     CITY: Denver
STATE: Colorado
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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APPLICANT: Grieve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 1
358 FKPKW 362
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STREET: 17
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US-08-639-075A-113
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APPLICANT:
APPLICANT:
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APPLICANT:
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February 27, 2002, 11:54:08 : Search time 62.61 Seconds
(without alignments)
11.681 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                   protein - protein search, using sw model
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sp_invertebrate:*
sp_mammal:*
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I FPXWR 5
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1: sp_archea:*
2: sp_bacteria:*
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sp_phage:*
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES		Description	Q9v671 drosophila	Q39293 brassica na	Q9xty5 caenorhabdi	Q9nnw3 homo sapien	Q9nnw2 homo sapien	Q37633 rhaqoletis	Q9pdel xylella fas	Q9suv9 arabidopsis	Q9ht83 pseudomonas	Q9d617 mus musculu	Q9apj5 erwinia chr	Q913g9 erwinia rha	Q9ftm4 oryza sativ	Q15429 homo sapien	O9saal arabidopsis	O9fdk4 zymomonas m	086742 streptomyce	09i702 pseudomonas	O16923 caenorhabdi
SUMMARIES		9	 09v671	039293	09xTY5	O9NNW3	Q9NNW2	037633	Q9PDE1	680860	Q9HT83	0911617	Q9APJ5	091369	Q9FTM4	Q15429	Q9SAA1	Q9FDK4	086742	091702	016923
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		Suery Match Length DB	101	113	157	1.58	1.58	229	245	273	292	321	332	333	334	349	417	466	479	497	501
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		Score	53	58	29	29	29	29	29	58	29	29	53	29	53	53	53	29	29	29	29
		Kesult No.	-	7	m	₹	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19

099415 caenorhabdi 029748 archaeoglob 09brq1 homo sapien 09h8y2 homo sapien 09h8y2 homo sapien 066676 aquirex aeo 09nw19 homo sapien 09nw19 homo sapien 095396 helicobacte 017366 caenorhabdi 09bw2 homo sapien 09dx4 mus musculu 09dx4 mus musculu 09dx4 mus musculu 09dx4 bordetella 04534 bordetella 04536 bordetella 0747471 synechocyst 074471 synechocyst 07478 synechocyst 09m045 arabidopsis	N.I. S.	01 AA.	ated) t sequence update) t annotation update)	ata: Hexapoda: Insecta: ptera: Brachycera: Muscomorpha;	Evans C.A., Gocayne J.D., , Hoskins R.A., Galle R.F., Ashburner M., Henderson S.N.,	.G., Champe M., Pfeiffer B.D., G., Nelson C.R., Miklos G.L.G., rews-pfannkoch C., Baldwin D., yraktarogiu L., Beasley E.M., Bhandari D., Rolshakov S.,	okstein P., Brottier P., dieu E., Center A., Chandra I., enport L.B., Davles P., s A.D., Dew I., Dietz S.M., -Rocha S., Dunkov B.C., Dunn P., C., Ferriera S., Fleischmann W., Gelbart W.M., Glasser K.,	A Nodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., A Marris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Bratin D., Houston K.A., Howland T.J., Wel MH., Ibegwam C., A Minnell B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., B. Hasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., A Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Abrkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
8.0	LIGNMENT		ed) seque annot	'ly). Tracheate ota: Dipte sophila.	.A., P.W. S.,	selt And And P.	Cav Cav Dav May Dugan	Gu Z J., H F.J., Ke, Kr Li, J. McLe
09GUI5 029748 029BRQ1 09HBY2 06HBY2 069WI9 09OWN19 09DZLF3 091ZF3 091ZF3 091ZF3 091ZF4 091ZF4 091ZF4 091ZF4 091ZF7	⋖	PRT	രാഗര	+ b.c.	731132, 40lt R 3., Li chards	E.G., 1 H.J.: Jale J	cler H Liber H Like C. eng Z. s M., I	J.H., nan T., Aland ' G.H. raft C A.A., T.C., Mobar
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		ELL	LEM NEW	azo pte pros	N.A 2Y; 206; 206; elni 30; ewi:	Rogie C lbay Basu Seno	Susar Sawl Sawl Del Ip L	ng F larvisto lush (odi Y.,
		2	10 T	mel Met Nec a; D	KECE 1960 1960 P.C	C. γ Doy 1 γ Ag	B	Gor Hou Kal Kal Let Let
88888866666666666666666666666666666666		/671 /671	-MAY-200 -MAY-200 -57N-200	Drosophila melanogaster (Fruit Elvaryota: Metazoa: Arthropoda Pleryota: Webptera: Endoptery Spindfoidea: Drosophilidae; Dro VGS: _TaxID-7227;	JUENCE F RAIN=BER DLINE=20 DMS M.D. AMS M.D. AMSTIGES DYGE R.A	n K.H., ril J.F. liew R.M	rekova D. reis K.C erry J.M Pablos Hoon K., chin K.J	odek A., rris N.E. stin D., lali M., muel B.E. sko P., i X., Ma
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Caenorhabditis elegans.
                                                                        SEDUENCE FROM N.A.
                                                                                                                    SEQUENCE FROM N.A.
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40 FPAWR 44
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SEQUENCE
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Mount S.M., Moy M., Murphy B., Murphy I., Muzny D.M., Nelson D.L.,
A Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J. Puri V. Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue D.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
A Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
A SVIRSkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
A Lillams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Candy X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
A Chos R.H., Myers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.";
EMBL, Ae003823, AAFS85601;
BENL, AE003823, AAFS85601;
BENL, AE003823, AAFS85601;
BENL, AE003823, AAFS85601;
BENL, AE003823, AAFS85601;
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                         Score 29; DH 5; Length 101.
Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 AA; 12560 MW; 149783D707223948 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U21744; AAA86366.1;
Mcndcl; 15767; Hrana;1139;15767.
InterPro; 1PR000795; CTP_EFTU.
Elongation factor; GTP-binding; Protein biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2PROTEIN.
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Last annotation update)
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80.0%;
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Best Local Similarity Bu.v.
And 4; Conservative
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Best Local Similarity 80.0
Matches 4: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-3708;
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75 FPAWR 79
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Kushhara K., Sasaki Y., Nakao F., Ihara K., Hattori H., Yamashita S., Nikei K., Koide N., Aiba H., Takeshita K., Hara T.; Asatysis of measles virus binding sites of the CD46 gene in patients with subacute sclerosing panencephalitis."; J. Infect. Dis. 181:1447-1449(2000).
                                                                                                                                                                                                                                                                                                                                                 Coulson A.,
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilida; Rhabdiloidea;
Rhabdilidae; Peloderinae; Caenorhabdilis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                         Wilson R., Ainscough R., Maderson K., Baynes C., Berks M., Berfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A. Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L., Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M., Farsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Yaudin M., Vaudihn K., Vaudihn K., Walerston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                  Mo:timore B.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6C6A837282EEB26C CRC64;
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Pred. No. 1.9e+02;
0; Mismatches 1;
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Interpro: IPRO00230; Ribosomal_S12.
Prim: PF00164; Ribosomal_S12: 1.
PRINTS; PR01034; RIBOSOMALS12.
Probom: PD000576; Ribosomal_S12: 1.
SECUENCE 157 AA; 17370 WW; 6C6A
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80.0%;
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SMART; SM00032; CCP; 2
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Best Local Similarity
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158 1
158 AA;
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Length 158;

Score 29; DB 4;

96.78;

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FERRICYTOCHROME C.
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Matches 4, Conserv
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SEQUENCE
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MEDLINE-97159559; PubMed-9007018;
MEDLINE-97159559; PubMed-9007018;
MILL J.J., Bush G.L.;
Phylogeny of the grous Rhagoletis (Diptera: Tephritidae) inferred from DNA sequences of mitochondrial cytochrome oxidase [1.";
MOI. Phylogenet. Evol. 7:33-43[1997].
I-FUNCTION: CYTOCHROME C OXIDNSE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2
TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA IT'S BINGGLEAR COPPER
A CENTER TO THE HIMFTALLIC CENTER OF THE CATALYTIC SUBUNIT 1 (BY
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Nihal ysis of measles virus binding sites of the CD46 gene in patients with subacute sclerosing panencephalitis.";
J. Infect. Dis. 18:1447-1449(2000)
InterPro. [PR000436.1;
InterPro. [PR0004436.1;
Pfam; PF00084; sushi, 2.
SMART: SM00032; CCP: 2.
SMART: M00032; CCP: 2.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annolation update)
COT-JUN-2001 (TREMBLREL. 17, Last annolation update)
COTIOCHROME C OXIDASE POLYPEPTIDE 11 (EC 1.9.3.1) (FRAGMENT).
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   Pred. No. 1.9e-102;
0; Mismatches 1; Indels
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEMBRANE COFACTOR PROTEIN CD46 VARIANT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                 158 AA.
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80.08;
                                       Conservative
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Matches 4; Conservative
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Matches 4; Conserv
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                                                                                                                                                                                  .. COFACTOR: COPPER A AND HEME GROUP.
SIMILARITY).
-:- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barteria; ProLeobacteria; gamma subdivision; Xanthomonas group; Ythella.
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0
                                                                                                                                                                                                                                                                                            INNER MEMBRANE (BY SIMILARITY).
SIMILARY: TO THE CYTCCHROME C OXIDASE SUBUNIT 2 FAMILY.
EMILY: US3254: AA850355.1; -.
ISSP: P08306: 1AR1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This property of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229
26389 MW; 912D1B2736330698 CRC64;
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Last annotation update)
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COPPER A (PROBABLE).
COPPER A (PROBABLE).
COPPER A (PROBABLE).
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01-00T-2000 (TrEMBLrel. 15, Last seq
07-MAR-2001 (TrEMBLrel. 16, Last ann
HYPOTHETICAL PROTEIN XF1438.
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garbor R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen IT., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAOI, an
                                                                    Pseudomonas aeruginosa.
Bacteria: Proteobacteria: gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPRO00504; RRM.
PROSTIE; PS00030; RRM_RNP_1; UNKNOWN_1.
[kjpothetical protein; Complete proteome
SEQUENCE 292 AA; 32949 MW; 14610337E8CCDFD4 CRC64;
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Pred. No. 3.3e+02;
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                                                                                                                                                                                                                                     STRAIN-PAO1;
MEDLINE-20437337; Pubmed-10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL: AE004961; AAG08873.1; -.
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              HYPOTHETICAL PROTEIN PA5488
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Best Local Similarity
Matches 4: Conservat
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                                                                                                                                                       NCBI_TaxID=287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 FPSWR 235
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                                                                                                                           Pseudomonas
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                        Gaps
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da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H., Van Sulys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zalz M., Meldanis J., Setubal J.C.; The genome sequence of the plant pathogen Xyiella fastidiosa."; The genome sequence of the plant pathogen Xyiella fastidiosa."; Mature 406:151-159(2000).

EMBL, AE003974; AAF84247.1; -. Hypothetical protein. Complete proteome.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.7%; Score 29; DB 10; Length 273; 80.0%; Pred. No. 3.1e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                  Length 245;
                                                                                                                                                                                                                                                                                                         96.7%; Score 29; DB 2; Length 245
80.0%; Pred. No. 2.8e+02;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

BEVAN M., Wedler H., Wambutt R., Bancroft I., Mewes H.W.,
MAYOF K.F.X., Lemck K., Schucller C.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ dalabases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL033545; CAA22165.1; -.
EMBL; AL16155; CAB79215.1; -.
Hypothetical protein.
SEQUENCE 273 AA; 31248 MW; 7E644F686CE8EBB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FU Arabidopsis sequencing project;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 31 2 FAB PROTEIN
F7K2.180 OR AT4G22600.
Arabidopsis thaliana (Mouse-car cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                         Ouery Match 5 96.7 80st focal Similarity 80.0 Matches 45 Conservative
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 FPSWR 201
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79 FPSWR 83
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01-MAR-2001 (
01-JUN-2001 (
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Length 292;

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MEDLINE-21085660; PubMed=11217851;

MEDLINE-21085660; PubMed=11217851;

A Arawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arawa T., Hara A., Eukunishi Y., Konno H., Adachi J., Fukuda S.,

A Arawa T., Hara A., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Salto T., Okazaki Y., Gojobori T.; Bono H., Rasukawa T., Salto R.,

RA Arawa T., Hara A., Saburner M., Batalov S., Casavant T.,

RA Arawa K., Isawa M., Nishi K., Kiyosawa H., Koodo B., Kooliwa H.,

Radola K., Matsuda H.A., Salton R., Batalov S., Casavant T.,

RA Kuehl P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schrimi L.M., Staubli F., Suzuki R., Tonirola M., Wagner L., Washio T.,

Schrimi L.M., Staubli F., Suzuki R., Tonirola M., Wadnerli R.,

Baske J., Boffelli D., Bojunga N., Carninci P., de Honaldo M.F.,

Baske J., Boffelli D., Bojunga N., Carninci P., de Honaldo M.F.,

Baske J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Cymns P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Acridone P., King B., Ringwald M., Rodrigucz I., Sakamocto N.,

Asasaki H., Sato K., Schoenbach C., Schoenbach C., Whittaker C., Wilming L.,

Wasanaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Wasanaki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L.,

Wasanaki H., Sato K., Schoenbach C., Kawaji H., Kohtsuki S.,

Wasanaki H., Sato K., Schoenbach C., Kawaji H., Kohtsuki S.,

Wasanaki H., Toyo-oka K., Wang K.H., Weltz C., Wawaji H., Kohtsuki S.,

Wasanaki H., Sato K., Satosuka K., Rawaji H., Kohtsuki S.,

Wasanaki H., Sato K., Satosuka Y., Kawaji H., Kohtsuki S.,

Wasanaki H., Sato K., Satosuka Y., Kawaji H., Kohtsuki S.,
      Gaps
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Mammalia, Eutheria, Rodentia, Sclurognathi, Muridae, Murinae, Mus.
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1; Indels
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Last annotation update)
0; Mismatches
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RESULT 09HT83

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us-09-446-109a-23.rspt

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possess genes homologous to the type II secretion pathway."; S::bmltted (MAY-2000) to the EMBL/GenBank/DDBJ.databases.
EMH: AJ276358; CA889803.1; .
InterPro: IPR002037; GIyco_hydro_8.
Pran: PF01270; GIyco_hydro_8.
Pran: PF01270; GIyco_hydro_8.
PRN: PF01270; GLHYDRLASE8.
                                                                                                                                                                               Signal; Hydrolase; Glycosidase.
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Best Local Similarity 80.0
Matches 4: Conservative
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Best Local Similarity 80.6
Matches 4; Conservative
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ID Q15429
AC Q15429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                      Gaps
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Pectobacterium.
NCBI_TaxID=556;
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                                                                                                                                                                            96.7%; Score 29; DB 11; Length 321;
80.0%; Pred. No. 3.7e+02;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.7%; Score 29; DB 2; Length 332; 80.0%; Pred. No. 3.8e+02; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF282321; AAG49556.1; .
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
MGD; MGI:1919189; 2310076014R1k.
Interpro; IPR000847; HTH_LYSR.
PROSTTE; PSUDA44; HTH_LYSR.FSR.ILX; UNKNOWN_I)
SEQUENCE: 321 AA; 35038 WW; 6E27EBC746552DFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL 1 23 POTENTIAL.
SEQUENCE 332 AA; 37627 MW; A1B5D7B0CBB20EE6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENDO-1,4-BETA-D-GLUCANASE PRECURSOR.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update).
01-JUN-2001 (TrEMBLrel. 17, Last annotation update).
ENDOCLUCANASE PRECURSOR (EC 3.2.1.4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 AA.
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Best Local Similarity 80.0
Matches 4; Conservative
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Matches 4; Conservative
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01-0CT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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178 FPAWR 182
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09APJ5
AC 09APJ5
DT 01-JUN
DT 01-JUN
DE ENDO-1
GN CELBY.
OC BECCED
OC BECCED
OC PECTOD
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AC 091.3G9
DT 01-0CT-
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Skaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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STRAIN-CV. NIPPONBARE;
STRAIN-CV. NIPPONBARE;
SASSAL T., MALSUMOLO T., Yamamoto K.;
"Cryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0005A05.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AP002863; BAB16921.1; -
InterPro: IPR000520; Exonuclse.
interPro: IPR000822; Znf-C2H2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 334;
                                                                                                                       Length 333;
                                                                                                                    96.7%; Score 29; DB 2; Length 333
80.0%; Pred. No. 3.8e+02;
tive 0; Mismatches 1; indels
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SMART: SM00355; ZnF_C2H2; 2.
PROSITE; PS30028; ZINC_FINGER_C2H2_1; UNKNOWN_1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; I.
SMOUGHQE: 334 Aa; 37172 MW; A34531D625704A88 CRC64;
                                                333 AA; 37783 MW; D75CFF212302673A CRC64;
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Last annotation update)
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Last annotation update)
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80.0%; Pred. No. 3.8e+02;
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                           ENDOCLUCANASE.
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POTENTIAL.
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01-MAR-2001 (TrEMBLrel. 16, Last scq.
01-JUN-2001 (TrEMBLrel. 17, Last ann
P00.05A05.25 PROTEIN.
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51-NOV-1996 (TriMBLrel. 01, Last seq.
31-JUN-2001 (TriMBLrel. 17, Last ann
CD46.
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Search completed: February 27, 2002, 11:54:08 Job time: 228 sec

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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae:
eurosids II: Brassicales; Brassicaceae; Arabidopsis.
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Vysotskala V.S. Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Li J., Lee J.M., Kremenetskala I., Liuros J., Ngan I., Liu A.,
Gonzalez A., Altelf H., Araujo R., Chao O., Conn L., Conway A.B.,
Dunn P., Hansen N., Huizar L., Kim C., Palm C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federsplat N.A., Theologis A.,
"Arabidopsis thaliana chromosome I BAC F25C20 sequence.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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80.0%; Pred. No. 4.7e+02;
rative 0; Mismatches 1; Indels
                                                                            TISSUE-TESTIS:
Hara T., Suzuki Y., Nagasawa S., Seya T.:
CDNA cloning and characterization of human sperm CD46.";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: D84105; BAA1224.1;
HISSP: P10998; 1VVD.
Interpro7, 1PH0004316, Sushi_SCR_CCP.
Fram: PP00084; sushi; 4
SMART: SM00012; CCP; 4.
SEQUENCE 349 AA: 39325 MW; BEFCEDA30D3C818E CRC64;
                                                                                                                                                                                                                                                                    96.7%; Score 29; DB 4; Length 349;
80.0%; Pred. No. 4e+02;
live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMHL: AC007296; AAD30247.1; -.
SEQUENCE. 417 AA: 45985 MW; B86EBF06AC19A63D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1999) to the EMBL/GenHank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                            09SAA1;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
F25C20.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                417 AA.
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The A; Conservative
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Matches 4; Conservative
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Theologis A.;
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STRAIN-CV. COLUMBIA;
Theologis;
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                                 NCBI_TaxID-9606;
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11 FPSWR 15
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109a-23.rsp

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(without alignments)
7.825 Million cell updates/sec
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                                                                                                                                                                               February 27, 2002, 11:51:50; Search time 66.26 Seconds
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/ SIDSB/gcgdata/geneseq-geneseqp/AA1992.DAT:
/ SIDSB/gcgdata/geneseq-geneseqp/AA1993.DAT:
/ SIDSB/gcgdata/geneseq-geneseqp/AA1995.DAT:
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1: /S10SB/gcgdata/yenescqp/AA1980.DAT:*
2: /S10SB/gcgdata/yenescq/yenescqp/AA1981.DAT:*
3: /S1DSB/ycgdata/yenescq/yenescqp/AA1981.DAT:*
4: /S1DSB/ycgdata/yenescq/yenescqp/AA1983.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         522463 seqs, 74073290 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB scq length: 2000000000
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Result		Query				
9	Score	Match	Match Length DB	DB	(11)	Description
-	32	88.9	39	20	AAW74031	Human D2H binding
7	32	88.9	392	7.7	AAG21559	Arabidopsis thalia
'n	32	88.9	399	21	AAG21558	Arabidopsis thalia
~	32	88.9	588	21	AAG47006	Arabidopsis thalia
S	32	6.88	594	21	AAG47005	Arabidopsis thalia
و	29	90.6	143	2	AAY92706	Geminivirus Rep C2
7	29	90.6	179	21	AAG58145	Arabidopsis thalia
æ	53	80.6	179	21	AAG60688	Arabidopsis thalia
6	53	9.08	179	2.1	AAG60692	Arabidopsis thalia
2	29	9.08	287	2 1	AAG59876	Arabidopsis thalia
Ξ	59	9.08	335	71	AAY92318	Mastrevirus Rep in

WPT: 1999-009568/01.

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3	80.	4	21	690	dopsis
4 2	80.	343	21	AAG58144	Arabidopsis thalia
2	80.	S	20	36	Protein involved i
1: 28	. 7.	7.1	22	582	#326
2	77.	7.1	22	AAM29310	-
7	77.	71	22	153	Peptide #3220 enco
7	77.	82	21	306	Human sccreted pro
2	7.7	\circ	21	307	Eucalyptus grandis
2	7.7	\circ	20	323	Human osteoprotege
~	.7.	~	17	4	Mutated OCIF, OCIF
2	77.	7	21	3	Human ORFX ORF903
7	77.	\sim	11	4	Mutated OCIF, OCIF
7	77.	2	17	4	Mutated OCIF, OCIF
7	. 77	~	20	2	THMA-07
2.7 28	77.8	351	17	AAR99943	
7	77.	ıO	22	88	-
7	77.	iO	22	36	Human EST encoded
7	17.	10	22	88	-
7	77.	'n	11	33	OC1F,
7	77.	LO.	11	33	Mutated OCIF, OCIF
7	77.	S	17	33	
7	77.	Ω	17	33	OCIF,
7	77.	ന	17	AAR99924	Mature osteoclasto
7	. 77	ന	22	8	Murine OPG cystein
7	. 77	ന	22	342	Rat Gasl protein.
7	77.	CD.	17	935	nec
7	77.	G	13	323	F ge
7	77.	3	21	555	thal
7	77.	S.	21	522	Zea mays protein f
7	77.	do.	17	994	d OCIF,
7	77.	g.	19	763	Modified TR1 recep
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T\$04/M&% CT	Standard;	peptide;	e ;	39 AA.	

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93.1. hPEPT1; human; GI tract receptor; sucrose-isomaltase complex; statestinal peptide-associated transporter; hyperlension; diabetes; ostcoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris; therapeutic agent delivery; therapy.
                                                                                           Gas mo-intestinal transport receptor; binding protein; hSI; HPTI;
                                                                                                                                                                                                                                                                                                                                                  Lambkin IJ;
                                                                                                                                                                                                                                                                                                                                                 Cagney GM, Carter JM, , Singleton J;
                                                              Regan D2H binding protein DAB3.
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Patterson CA,
                                      1- -MAY-1999 (first entry)
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omaliony DJ,
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99US-0139458.
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99US-0139460.
                                    99US-0132407.
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99US-0132485.
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   This sequence represents a peptide that specifically binds to the human D2H protein. The invention relates to purified proteins (1) that bind specifically to at least one of the gastro-intestinal (61) tract receptors human intestinal peptide-associated transporter (HVTI).

**Reproduction intestinal peptide-associated transporter (HVTI).

**Reproduction by the repeutic agents through human and animal GI tissue (into the blood) for in vivo delivery, particularly for treatment or prevention of hypertension, diabetes, osteoporosis, haemophilia, anaemia, cancer, migrande, or angina pectoris. Specifically they are used to cancer, migrande, or angina pectoris. Specifically they are used to are disclosed, including genes or inhibitory nucleic acid, imaging agents and antigens. (1) may also provide targeting to the GI tract. Other uses of (1) are: (1) to determine the level of specified receptors in a sample (in a binding assay); and (ii) to screen for molecules that bind (1). Immunogenic analogues or derivatives of (1) are used to raise antibodies and in immunosasays. The antibodies are used to locate, detect and measure (1), e.g. for imaging monitoring treatment, tissue analysis etc., also for peptide purification and immobilisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
New proteins that bind specifically to receptors in the gastro-intestinal tract and related nucleic acid - chimmeras and antibodies, used to deliver therapeutic or diagnostic agents to, or through, the gastrointestinal tract, e.g. insulin or leuprolide
                                                                                                                                                                                                                                                                                                                                                      Ouery Match 88.9%; Score 32; DB 20; Length 39; Best Local Similarity 71.4%; Pred, No. 7; Matches 5; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 24159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC21559 standard; Protein; 392 AA
                                                             Claim 2; Page 54; 294pp; English.
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990S-0128714.
990S-0129845.
990S-0130077.
990S-0130449.
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99US-0126264.
99US-0126785.
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9903-0150884.
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26-JUL-1999;
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990S-0121825 990S-0123180 990S-0125788 990S-0126764 990S-0126765 990S-0126765 990S-0128714 990S-0128714 990S-0130077 990S-0130891 990S-0130891 990S-0130891 990S-0130891 990S-0130891 990S-0130891 990S-0130891

25 - VEB - 1999 05 - MAR - 1999 09 - MAR - 1999 25 - WAR - 1999 27 - WAR - 1999 06 - APR - 1999 06 - APR - 1999 15 - APR - 1999 15 - APR - 1999 21 - APR - 1999 21 - APR - 1999

23-APR-1999; 23-APR-1999; 28-APR-1999;

30 .. APR-1999; 04 .. MAY-1999; 05 - MAY-1999; 05 - MAY-1999;

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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0; Mismatches
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99US-0159638.
99US-0160741.
99US-0160761.
99US-0160770.
99US-0160770.
99US-0160814.
99US-0160980.
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Best Local Similarity
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118 kfgpkwr 124
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AAG47006
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                  AAG58145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The geminivirus rep gene sequence contains a Cl open reading irame (ORF) which encodes RepA. Rep is the translation product of the spliced Cl and CZ ORFs. Upon transcription and translation, the expressed protein replicase can act in trans to effect rescue and replication of a desired heterologous nucleotide sequence. A pair of nucleic acids comprising a portion of a long intergenic region (LIR) of a geminivirus genome lacking a sequence encoding a geminiviral coal protein, and a nucleic acid comprising a geminiviral replicase gene linked to a fruit ripening dependent promoter, are new. Strains of Escherichia coll and Astrobacterium tumefaciens transfected with an expression vector the production of transgenic plants (or cells). The sequences and methods are useful for amplifying a gene of interest and overproducing a protein
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids comprising a portion of a long intergenic region of a genthivitus genome and a sequence comprising a geniniviral replicase gene, useful for amplifying a gene of interest and overproducing a protein of interest in plants
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                                                                                                                                                                                                                                                                                                      Rep; replicase; rescue; replication; vector; gene expression; recombinant protein production; plant.
   Length 594;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heiferon KL, Arntzen C;
Score 32; DB 21; L
Pred. No. 1.1e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 10; 121pp; English.
                                                                                                                                                                         AAY92706 standard; Protein; 143 AA.
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88.9%;
71.4%;
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Ouery Match 88.9
Best Local Similarity 71.4
Matches 5; Conservative
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N-PSDB; AAA09238.
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|124 kfgpkwr ||30
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                                                               1 KFXPXWR 7
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                Arabidopsis thaliana protein fragment SÉQ 10 NO: 75022
AAG58145 standard; Protein; 179 AA.
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99US-0134219.
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99US-0139119.
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99US-0134370.
99US-0134768.
99US-0134941.
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99US-0136392
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99US-0137724
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                                 (first entry)
                                                                                   termination sequence.
                                                                                                  Arabidopsis thaliana.
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07-MAY-1999;
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06 NPR-1999;
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Score 29; DB 21; Length 143; Pred. No. 1e+02; 1; Mismatches 2; Indels

80.6%;

4; Conservative

Best Local Similarity Matches 4; Conserv

Query Match

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1 KFXPXWR 7

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PR 18-UN-1999 9919-0133458
PR 18-UN-1999 9919-0133458
PR 18-UN-1999 9919-0133458
PR 18-UN-1999 9919-0133458
PR 22-UN-1999 9919-0139450
PR 22-UN-1999 9919-0139750
PR 22-UN-1999 9919-0140854
PR 22-UN-1999 9919-0140854
PR 22-UN-1999 9919-0140854
PR 22-UN-1999 9919-0140854
PR 22-UN-1999 9918-014184
PR 22-UN-1999 9918-0141834
PR 22-UN-1999 9918-0144884
PR 24-UN-1999 9918-0144884
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·	Length 179; Indels	
	29; DB 21; No. 1.3c+02; ismatches 2;	
	Score 29, Pred. No 0; Mismat	
90.5 - 0149929.9 90.5 - 0149929.9 90.5 - 0149929.9 90.5 - 0149929.9 90.5 - 0150884.9 90.5 - 0151086.9 90.5 - 0151086.9 90.5 - 0151089.9	80.68; ty 66.78; ervative	
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20 - Aug 22 - Aug 23 - Aug 24 - Aug 25 - Aug 26 - Aug 27 - Aug 27 - Aug 27 - Aug 28 - Aug 29 - SEP 20 - S	Query Match Best Local S Matches	× -
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Gaps

AAGSO688 standard; Protein; 179 AA.

RESULT 8 AAG60638 1D AAG50688 XX AC AAG40688

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02-AUG-1999;
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11-AUG-1999;
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   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                              Arabidopsis thaliana protein fragment SEQ ID NO: 78638
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18-OCT-2000 (first entry)
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Pred. No. 1.3e+02;
0; Mismatches 2; Indels
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99US-0160980.
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990S-0161993
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PR 29-7/10-1999; 9908-01410287

PR 01-7/10-1999; 9908-01410287

PR 01-7/10-1999; 9908-01410287

PR 01-7/10-1999; 9908-0142020

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PR 20-7/10-1999; 9908-014909

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Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
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for use in the invention. Removal of the introm greatly enhances bean yellow dwaff virus replication. Upon transcription and translation, the expressed protein replicase can act in trans to effect rescue and replication of a desired heterologous nucleotide sequence. A pair of nucleic acids comprising a portion of a long intergenic region (LIR) of a geminivirus genome lacking a sequence encoding a geminiviral coat protein, and a nucleic acid comprising a geminiviral replicase gene linked to a fruit ripening-dependent promoter, are new. Strains of Escherichia coli and Agrobacterium tumefaciens transfected with an expression vector containing the nucleic acids and a gene of interest are useful for the production of transgenic plants (or cells). The sequences and methods are useful for amplifying a gene of interest and overproducing a protein of interest in recombinant plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; melabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                   This is the product of an intronless rep gene sequence from Mastrevirus
                                                           Nucleic acids comprising a portion of a long intergenic region of a genuinivirus genome and a sequence comprising a geniniviral replicase gene, useful for amplifying a gene of interest and overproducing a procein of interest in plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 80.6%; Score 29; DB 21; Length 335; Best Local Similarity 57.1%; Pred. No. 2.5e+02; Matches 4; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                          Disclosure, Fig 18; 121pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 287;
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); Mismatches 2;
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llarity 66.7%; Prod. No. 2.1e+02;
Conservative 0; Mismatches 2.
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Pred. No. 2.5e+02;
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                                                                                                                                                                                                                                                                                                                                              AAG60691 standard; Protein; 342 AA
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9905-0123180
9905-0125788
9905-0126264
9905-0126785-
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990S-0131449
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99US-0132486
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nes 4; Conservative
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233 kfspaw 238
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 2.5e+02;
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99US-0123180.
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233 kfspaw 238
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21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                Vaccine; eye disease: conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
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                                                                                                   Score 29; DB 21; Length 343;
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            990S-0161361.
990S-0161920.
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990S-0161993.
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Score 29; DB 20; Length 354; Pred. No. 2.6e+02; 1; Mismatches 2; Indels

Ouery Match
Best Local Similarity 57.1%;
Matches 4: Conservative

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

February 27, 2002, 11:52:58; Search time 34.86 Seconds (Without alignments) 15.296 Million cell updates/sec Run on:

US-09-446-109A-24 36 1 KFXPXWR 7

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 rotal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARLES

1.ES	Description.	70K protein - pota	othetical p	O	hypothetical prote			S	replication-associ	replication-associ	conserved hypothet	SPOI4 protein - ve	cha	hypothetical prote	_	,	•	hypothetical prote		hypothetical 38.5	probable sulfite s	conserved hypothet	ubiquinol cytochr	probable integrase	conserved hypothet	hypothetical prote	cytochrome P450-li	probable anion exc	virulence-associat	transcription effe
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## ALIGNMENTS

RESULT 11  NAMONOTO (2) Species as potato leaf roll virus (strain 1)  A. Molta: Dota potato leaf roll virus (strain 1)  A. Molta: post potato leaf roll virus  A. Molta: post solanum tubersouum (potato)  C. Date: 11-Mar-1190 sequence_revision 31-Mar-1190 stext_change 21-Jul-2000  C. Maccasion (2) Molta: post solanum tubersouum (potato)  A. Molta: post solanum tubersoul tubersoul solanum tubersoul tubersoul solanum tubersoul tub
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Caps 0;

Score 33; DB 2; Length 639; Pred. No. 38; 0; Mismatches .2; Indels

Query Match 91.7%;
Best Local Similarity 71.4%;
Macches 5; Conservative

KEXPXWR 7

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C:Specings: Aeropyrum nernix
C:Specings: Aeropyrum nernix
C:Specings: Aeropyrum nernix
C:Date: 20-Aug-1999 #text_change 09-Jun-2000
C:Accession: 872549
K:Rawarabayasi, Y:; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Ta awa, H.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Ta awa, H.; Tanaka, T.; Kudoh, Y.; Vinanazaki, J. N.; Tanaka, T.; Kudoh, Y.; Vinanazaki, J. N.; Tanaka, T.; Kadarasi, J.; MulD:99310339
A:Tile: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerosession: B7249
A:Reference number: A72450; MulD:99310339
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1.254
A:Residues: 1.254
A:Residues: 1.254
A:Residues: 1.254
A:Residues: 1.254
A:Residues: ARAN>
A:Residues: ARAN>
A:Reperimental source: strain Kl
C:Genetica: Application A
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R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
R:, Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, S.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
hature (02, 761-768, 1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable phospholipase AL2939400 [imported] - Arabidopsis thaliana
M.Altacrate names: lysophospholipase homolog F12L6.6
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C.Accession: T00550; H84816
C.Accession: T00550; H84816
A.A. C.Cosby, M.L.: Brandon, R.C.; Sykes, Sibmit.ad to the EMBL Data Library, July 1998
A.Refirence number: 214168
A.Refirence number: 214168
A.Refirence number: 214168
A.Refirence number: ALACEST A.Refirence number: A.Refir
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                                                                                                                                                                                                                             BL:AL080282; GSPDB:GN00062; ATSP:T13K14.140 cultivar Columbia; BAC clone T13K14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothesical protein APE1678 - Aeropyrum pernix (strain KI)
submitted to the Protein Sequence Dalabase, June 1999
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                        A,Molecule type: DNA
A,Residues: 1-591 <BEV>
A,Cross-references: EMBL:AL080282;
A):Experimental source: cultivar Col
C,Genetics:
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71.48;
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                                 A; Reference number: 216991
A; Accession: T10640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matchus 5; Conserv
                                                                                                                                                                                                                                                                                                                                                          A;Gene: ATSP:T13K14.140
A;Map position: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 KFSPAWK 174
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C.Species: Arabidopsis thaliana (mouse-car cress)
C.Date: L6.Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C.Accession: T10640
R.Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke
                                                                                                                                                                                                Cormate hydrogenlyase, subunit 5 - Methanococcus jannaschii
Cispecies: Methanococcus jannaschii
Cispecies: Methanococcus jannaschii
Cispecies: Methanococcus jannaschii
Cispecies: 13-8pe-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
CiAccession: C64364
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.C.; Blake, Reich, C.I.; Overbeck, R.; Kirkness, E.F.; Weinstock, K.C.; Merrick, J.M.; Glodek, A.; Science 273: 1058-1073, 1996
A:Neince 273: 1058-1073, 1996
A:Neince 273: Saidow, P.M.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Heference number: A64300; MULD:96337999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Cross-references: GB:U67501; GB:L77117; NID:92826289; PIDN:AAB98504.1; PID:91591218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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A:Residues: 1-380 <BUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Arabidopsis thaliana (mouse-ear cress)
Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 24-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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0
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Pred, No. 37;
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A;Residues: 1-462 <DRA
A;Cross-references: EMBL;AF013294; NID:92252848; PID:92252849
A;Experimental source: cultivar Columbia
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T01549
hypothetical protein A_TM018A10.1 - Arabidopsis Lhaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #
C.Accession: "101549
R.Dempsey, S.: Marper, M.
submitted to the EMBL Data Library, July 1997
A. Reference number: 214348
A. Accession: "101549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.98;
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Best Local Similarity 71.4v
That 5; Conservative
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Host Local Similarity /1.4.4
Host Local Si Conservative
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A:Introns: 107/1: 143/2
A:Note: A_TM018A10.1
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327 KEPPSWR 333
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240 KFKPVWR 246
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1 KFXPXWR 7

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RESULT T10640

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A.Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pa A,Reference number: A82950; MUID:20437337
A.Accession: G83317
A.Status: preliminary
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A:Experimental source: strain PAOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein PA2630 [imported] - Pseudomonas aeruginosa (strain PAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Sperices: Pseudomonas aeruginosa
C:Dato: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: G83317
B:Stover, C.K.: Pham, X.Q.: Erwin, A.L.: Mizoguchi, S.D.: Warrener, P.: Hickey, M.J.: adman, S.: Yuan, Y.: Brody, L.L.: Coulter, S.N.: Folger, K.R.: Kas, A.: Larbig, K.: Nature 406, 959-964, 2000
                                                                                                                                                           A:Experimental source: Swedish isolate
A:Note: ORF 30156 and ORF 17292 are joined by removal of an intron in the region of
A:Note: the exact position of the intron is given in reference $71838
B:Scheik, H.J.; Matzeit, V.; Schiller, B.; Schell, J.; Gronenborn, B.
EMBO J. 8. 359-364, 1989
                                                                                                                                                                                                                                                                                   EMBO C. R. 359-364, 1989
A;Tituci Wheat dwarf virus, a geminivirus of graminaceous plants needs splicing A;Reference number: S71838; MUID:89251559
A;Contents: annotation: intron position
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C:Specius: Saccharomyces cerevisiae
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #tcxt_change 21-Jul-2000
C:Acnession: S38103; S57804
R:Urres:arazu, L.A.: Jauniaux, J.C.
submitted to the Protein Sequence Database, March 1994
A:Reference number: S38097
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A; Res.itues: 1-1683 - CURR>
A; Cross-references: EMBL:228256; NID:9486462; PID:9486463; MIPS:YKR031c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: towato golden mosaic virus AL1 protein C;Keywords: DNA replication
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Pred. No. 86;
1; Mismatches
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95;
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Pred. No.
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illarity 57.1%;
Conservative
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Best Inval Similarity 57.1
Matches 4: Conservative
                                                                                                                                 A;Cross-references: GB:X02869
         A; Reference number: A91012
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Best Local Similarity
The 4; Conserve
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A; Residues: 1-389 <STO>
                                   A;Accession: B24356
A;Molecule type: DNA
A;Residues: 1-351 <MAC>
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Alternate names: C1-1/C1-2 composite protein
C.Species: wheat dwaff virus
A.Variety: French isolate
C.Nate: 16-Fcb-1995 Esequence_revision 06-Dec-1996 #text_change 21-Aug-1998
C.Nates: 16-Fcb-1995 Esequence_revision 06-Dec-1996 #text_change 21-Aug-1998
C.Nacession: S4938
S.Nacession: S4938
A.Reference number: S7938
A.Reference number: S71838
A.Reference number
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: H84816
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EMBO J. 4, 2173-2180, 1985
                                                                                                                                                                              A;Cross-references: GB:AE002093; NID:93355469; PIDN:AAC27831.1; GSPDB:GN00139 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replication-associated protein - wheat dwarf virus (Swedish isolate)
N.Alternale names: ORF 30156/ORF 17292 composite protein
C.Species: wheat dwarf virus
A.Variely: Swedish isolaine
C.Date: 09-Sep-1987 #sequence_revision 06-Dec-1996 #text_change 21-Aug-1998
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A:Title: The nucleotide sequence of cloned wheat dwarf virus DNA
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86;
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Pred. No. 78;
1; Mismatches
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Pred. No. 6
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A;Introns: 55/1: 104/1: 147/3; 193/3; 226/3
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Similarily 57.1%;
4; Conservalive
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ilarity 57.1%;
Conservative
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Best Local Similarily
Matches 4; Conserv
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Hest Local Similarity
Matches 4; Conserv
                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-317 <STO>
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266 KFTPNWK 272
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167 KFIPTWK 173
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A:Title: The nucleotide sequence and genome structure of the geminivirus miscanthus s A:Reference number: JQ1355; MUID:92013947
A:Accession: JQ1359
A:Status: translation not shown
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A:Residues: 1:122 <PAR>
A:Cross:references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85265.1; PID:g738
A:Experimental source: serogroup A, strain 22491
C;Genetics:
                                                                           A;Cross-references: GB:AE002400; GB:AE002098; NID:97225659; PIDN:AAF40876.1; PID:9722 A;Experimental source: serogroup B, strain MC58 C;Genetics: A;Genetics: A;Gene: NMB0438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypotherical protein NMA2047 [imported] - Neisseria meningitidis (strain 22491 serogr C:Specias: Neisseria meningitidis ... C:Specias: Neisseria meningitidis ... C:Specias: No-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C:Accassion: C81775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P:Parkfill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo Horovd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Hature. 104, 502-506, 2000
A:Tille: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A:Reference number: A81775; MUID:20222556
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A:Resistes: 1-136 <CRA>
A:Resistes: 1-136 <CRA>
A:Cro-s-references: DDDJ:D01030
A:Cro-s-references: DDDJ:D01030
A:Note: Lhis reading frame extends between two stop codons and does not begin with a R:Chatani, M: Matsumoto, Y:: Mizuta, H:: Regami, M:: Boulton, M:: Davies, J:W. submitted to JTP1D, May 1991
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C2 processor - Miscanthus streak virus
C;Sperias: Miscanthus streak virus
C;Sperias: 30-Jun-1992 #sequence_revision 30-Jun-1992 #Lext_chauge 17-Nov-2000
C;Accession: J01359; J00922
C;Catcassion: J01359; J00922
F;Chatcas: M.; Matsumoto, Y.; Mizuta, H.; Ikcgami, M.; Boulton, M.I.; Davies,
J. Gen. Virol. 72, 2325-2331, 1991
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A; Accession: JQ0922
A; Motecale type: DNA
A; Residues: ", ", 2-136 CCH2>
C; Comment: Miscanthus streak virus causes leaf streak,
C; Super; amily: tomato golden mosaic virus ALI protein
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Pred. No. 50;
1; Mismatches
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50;
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Pred. No.
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
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     A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-122 <TET>
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A:Status: preliminary
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                                                                              A:TILLe: Commitment to melosis in Saccharomyces cerevisiae: involvement of the SPO14 gen A:Refedence number: S57804: MUID:9228685
A:Accession: S57804
A:Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                         A; Wolecule type: DNA
A; Residues: 304-1683 <HON>
A; Cross-references: EMBL:L46807; NID:q951462; PIDN:AAA74938.1; PID:q954831
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: EMBL:AL110469; PIDN:CAB54155.1; GSPDB:GN00066; SPDB:SPAC926.07c
A:Experimental source: strain 972h-; cosmid c926
C:Genetics:
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Cipate: 03-Dec:1999 isequence_revision 03-Dec-1999 #text_change 19-May-2000
CiAccession: T39205
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.
submitted to the EMBL Data Library, September 1999
A:Reference number: 221835
A:Reference number: 221835
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Pred. No. 3.7e+02;
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A;Cross-references: SGD:S0001739; MIPS:YKR031c.
A;Map postition: 11R
C;Function:
A;Description: required for meiosis and spore formation
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A:Molecule Lype: DNA
A:Residues: 1-85 <WOO>
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36;
A:Experimental source: strain S288C
R:Honigberg, S.M.; Conicella, C.; Espositio, R.E.
Genetics 130, 703-716, 1992
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Pred. No.
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A:Introns: 9/3: 21/1; 32/3; 65/1
C:Superfamily: dynein light chain
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 57.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1227 KFSPQWK 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KFXPXWR 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 KFSPTW 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KFXPXW 6
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0; Gaps
Query Malch 80.6%; Score 29; DB 2; Length 136; Best Local Similarity 57.1%; Pred. No. 56; Malches 4; Conservative 1; Mismatches 2; Indels
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1. KFXPXWR 7 11 | 1 : 59 KFLPQWK 65 q ò

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OM protein - protein search, using sw model

February 27, 2002, 11:52:17 ; Scarch time 20.39 Seconds
(without alignments)
12.587 Million cell updates/sec Run on:

US-09-446-109A-24 -36 Title: Perfect score:

1 KFXPXWR 7

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

100059 seqs, 36664827 residues Searched: 100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CHMMADIFC

		ø			SUMMARIES	
Kesult	3	Query		2	4	
	aloos	Match	reng cu	97	10	nordingen
-	34	94.4	639	_	V70K_PLRV1	
7	33	91.7	639	-	V70K_PLRVW	P11622 potato leaf
æ	32		459	-	KH1,2_KHOSH	
ಶ	32	88.9	591	-	1F37_ARATH	P56820 arabidopsis
S	30		1380	-	SP14_YEAST	
9	29		85	-	DYL1_SCHPO	Ogur05 schizosacch
7	29	80.6	146	-	Y17K_TYDVA	P31618 tobacco yel
æ	29	90.6	340	-	YHET ECOLI	P45524 escherichia
6	29		378	-	CYB_DROME	P18935 drosophila
10	29		452	_	SPS2_MOUSE	
11	29	80.6	477	-	YZ64_SYNY3	P73436 synechocyst
12	29		856	-	AAP1_YEAST	P37898 saccharomyc
13	28		136	-	Y16K_CSMV	P18919 chloris str
14	28		151	-	HSPD_BRAJA	_
15	28	-	151	-	HSPH_BRAJA	
16	28		153	_	HSPB_BRAJA	
17	28	77.8		-	YK110_YEAST	
18	28	77.8		-	VENV_BEV	P27904 berne virus
19	28	77.8		-	Y953_MYCTU	P71557 mycobacteri
20	28	77.8	333	-	DPSD_CAEEL	Q10949 caenorhabdi
21	28	77.8		-	GLPK_MYCLE	_
22	28	77.8		_	GLPK_MYC'rU	O69664 mycobacteri
23	28	77.8	554	~	ESTM_MOUSE	_
24	28	77.8		-	CD22_IIUMAN	P20273 homo sapien
25	28	77.8	943	-	SYI_PSEFL	P18330 pseudomonas
26	28	77.8		-	KRP1,_NDVB	P11.205 newcastle d
27	28	77.8	7	-	RRPI,_SV41	
28	27	75.0		-	Y18K_MSVK	
29	27	75.0		-4	Y18K_MSVS	_
30	.57	75.0		-	Y18K_MSVN	_
31	.27	75.0		-	YAF7_CAEEL	_
32	27	75.0		-	HO_FUGRU	073688 fugu rubrip
33	27	75.0	283	-	RUAL SOY HN	P39657 glycine max

P03955 macaca fusc	P20142 homo sapien	P32839 saccharomyc	P10635 homo saplen	Q29488 macaca fasc	018992 callithrix	Pl3108 rattus norv	064680 rattus norv	Q92113 squalus aca	023736 brassica ju	•••	P37629 escherichia
PEPC_MACFU	PEPC_HUMAN	BCS1_YEAST	CPD6_HUMAN	CPDH_MACFA	CPDJ_CALJA	CPD4_RAT	CPDI_RAT .	CPT7_SQUAC	GSH1_BRAJU	GSH1_ARATH	YH1L_ECOLI
-	_	-		_		_	_	-	_	-	-
377	388	456	497	497	497	200	200	509	514	522	535
15.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0
27	27	27	27	27	27	27	27	27	27	27	27
34	35	.35	3.7	36	. 63	2, C)		51	~	44	4.5

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                             01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
69-1, KDA PRUFIEN (ORF 2).
19-Otato leafroll virus (strain 1) (PLrV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                                                                                                                                                       MEDITINE-89279282; Pubmed-2732710; Ran L.; Robinson D.J., Jolly C.A., Hyman L.; Notleoctide sequence of potato leafroll luteovirus RNA."; Cen. Virol. 70:1037-1051(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.4%; Score 34; DH 1; Longth 639; 71.4%; Pred. No. 13; Eive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AttacPro: LPM000382; Luteo_ORF2.
多さm. PF02123; Luteo_ORF2.1.
※AKHTS: PR09131; LVIRUSORF2.
※AKHTRIS 619 AA: 69629 MW; AFCF2FB393BEE097 CRC64:
                                639 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMBL; D00530; BAA00417.1; -. 24BL; X14600; CAA32741.1; -. P!R JA0118; WWVQ70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best tocal Similarity 71.4
Matches 5: Conservative
                                STANDARD;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                       NCEL_TaxID-12046;
                             V70K_PLRV1
P17519;
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                V70K_PLHV1
SESOL
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014 KFTPSWR 620 : KFXPXWR 7 <u>...</u> õ

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of 6.22; % - 0.27-1989 (Rel. 12, Created) % - 0.27-1989 (Rel. 12, Last sequence update) % - 0.1-AUG-1990 (Rel. 15, Last annotation update) % - 7 KDA PROPELN (ORF. 2). % orato leafroll virus (strain Wageningen) (PLrV). 639 AA PRT; S'L'ANDARD; VZOK PERVW TO VZOK PERVW KESUL" TO DE CE

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FEST_ARATH
P55820:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                               use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen J.-II., Gibson J.L., MCCUE L.A., Tabita F.R.,
"Identification, expression, and deduced primary structure of
transketolase and other enzymes encoded within the form II CO2
fixation operon of Rhodobacter sphaeroides.";
J. Biol. Chem. 266:20447-20452(1991).
-! FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXXLATION OF
-! FIBULOSE I.5-BISPHOSPHARY THE PRIMARY EVENT IN PHOTOSYMTHETIC
CARHON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRACHENITATION OF
THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wagner S.J., Stevens S.E. Jr., Nixon B.T., Lambert D.H.,
Quivoy R.G. Jr., Tabita F.R.;
Nucleoride and deduced amino acid sequence of the Rhodobacter
sphaeroides gene encoding form II ribulose-1,5-biphosphate
carboxylase/oxygenase and comparison with other deduced forms I and II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caps
  ssRNA positive-strand viruses, no DNA stage; Luteoviridae;
                                                                                                                                                                                                                                FEDS LEUC. 245:51-56(1989).
                                                                                                                                            der Wilk F., Huisman M.J., Cornelissen B.J.C., Huttinga H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
                                                                                                                                                                                        "Nucleolide sequence and organization of potato leafroll virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1992 (Rel. 24, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RIBULOSE BISPHOSPHATE CARBOXYLASE LARGE CHAIN 2 (EC 4.1.1.39)
(RUBISCO LARGE SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.7%; Score 33; DB 1; Length 639; 71.4%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    639 AA; 69676 MW; 92E1473FE3FEF148 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEMS Microbiol, Lett. 55:217-222(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-36 FROM N.A.
MEDLINE-92041881; Pubmed-1939098;
                                                                                                                   MEDI,1NE-89171329; PubMed-2466700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S03547; S03547.
InterPro; IPR000382; Luteo_ORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y07496; CAA68795.1; -.
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PRINTS; PR00913; LVIRUSORF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rest Local Similarity 71.4
Matches 5: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                            NCBI_TaxID-12048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 | 11
614 KF1PSWR 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-1063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KFXPXWR 7
                                                                                                                                                                  Goldbach R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBBL2 OR RBPL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RBL2_RHOSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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DATE OF THE SET OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAN=CV. COLUMBIA:

STRAN=CV. COLUMBIA:

MEDLINE=20083488: PubMed=10617198;

MEDLINE=20083488: PubMed=10617198;

MEDLINE=20083488: PubMed=10617198;

MEDLINE=20083488: PubMed=10617198;

MEDLINE=20083488: PubMed=106.7198;

MEDLINE=20083488: PubMed=10.7. Merger M., Poil T., Merlis B., Ansorge M., Brandt P., Grivell L.A., Rieger M., Meller M., Meller M., Bancroft M., Melchert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft L., Merlis M., Dobbers J., Waldey P., Marsham S.-A., McCullagh B., Biltham L., Robben J., Vandenbussche F., Mellism S.-A., McCullagh B., Biltham Chuang Y.-J., Vandenbussche F., Mellism M., Wellisms I., Aert R., Defoor E., Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Mellisms P., Riein Lankhorst R., Rose M., Hauf J., Koetter P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3G-MAY-2000 (Rel. 39, Created)
3G-MAY-2000 (Rel. 39, Last sequence update)
2D-AUG-2001 (Rel. 40, Last annotation update)
PUSATIVE EUKARYOFIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 7 (EIF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fram: PF00016; RUBISCO_LARGE: 1.
PROSITE: PS00157; RUBISCO_LARGE: 1.
Procision for a carbon dioxide fixation; Photorespiration:
Lyase: Oxidoreductase; Monooxygenase; Multigene family.
ACT_SITE 191 BINDING OF CO(2) ACTIVATES THE ENZYME.
SECUENCE 459 AA; 50519 MW; 299ABAA836BD683E CRC64;
                                                                                                                             CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + 0(2) - 3-PHOSPHO-D-GLYCERATE + 2-PHOSPHOGLYCOLATE. SUBUNIT: IN CONTRAST TO FORM I GENES, THE FORM II RUBISCO ARE COMPOSED OF ONLY LARGE SUBUNITS.
REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                    MISCELLANGOUS: THIS PROTEIN IS ENCODED WITHIN THE FORM II RIBULOSE-BISPHOSPHATE CARBOXYLASE OPERON. SIMILARITY: BELONGS TO THE RUBISCO LARGE CHAIN FAMILY.
                                                                CATALYTIC ACTIVITY: D-RIBULOSE 1,5-BISPHOSPHATE + CO(2) 2 3-PHOSPHO-D-GLYCERATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.9%; Score 32; DB 1; Length 459; 71.4%; Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LaterPro; IPR000685; RuBisCO_large.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMDL; M68914; AAA26158.1; ALT_SEQ.
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AT4G20980 OR T13K14.140.
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Best Local Similarity
5; Conserve
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HSSP; P04718; 1RBA.
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OR PLINT OR YKR031C.

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RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Van Wonlegum M., Roders J., Cronin A., Quall M., Bray Allen S.,
RA Clark L., Doggett J., Itali S., Kay M., Lennard N., McLay K., Mayes R.,
RA Clark L., Doggett J., Itali S., Kay M., Lennard N., McLay K., Mayes R.,
RA Clark D., Blocker H., Scharfe M., Grimm M., Lochmert T.-H.,
Bose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA Cabel C., Fuchs M., Fartmann B., Grandcrath K., Dauner D., Herzl A.,
RA Achabl S., Hiller R., Schaidt W., Lecharny A., Aubourg S.,
RA Cibbons T., Weber C., Monfort A., Casacuberta E.,
RA Cibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Cibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Cibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Erishman D., Habses D., Lemcke K., Mewes HI.-W., Stocker S.,
RA Zaccarla P., Bevan M., Wilson R. K., de la Bastide M., Haberman K.,
RA Schon M., Wulson R. K., de la Bastide M., Haberman K.,
RA Schon M., Wulson R. K., de la Bastide M., Haberman D.,
RA Latrellle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Kamer J., Fulton L., Mardis E., Dante M., Pepin K.,
RA Ramer J., Fulton L., Mardis E., Dante M., Maleco A., Shah R.,
RA Antonolu B., Stoary A., Rodriguez M., Hoffman J., Till S.,
RA Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Wordan C.,
RA Antonolu B., Shody N., Hasegawa A., Hamed C., Lodhi M., Johnson A.,
RA Grant S., Shody N., Hasegawa A., Hamen C., Merco T., Kenp.
RA Antonolu B., Scholl W., McCombie W.R.,
Radis E., Martiensson R., Wiccombie W.R.;
Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIF3 (BY SIMILARITY).
SUHUNIF: EIF-3 IS COMPOSED OF AT LEAST 10 DIFFERENT SUBUNITS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:769-777(1999).
-I- FUNCTION: BINDS TO THE 40S RIBOSOME AND PROMOTES THE BINDING C
METHIONYL-TRNAI AND MRNA. ASSOCIATES WITH THE SUBUNIT P170 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n; Initiation factor; Protein biosynthesis.
66724 MW; 9C5E673F04E9845C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 1; Length 591;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AL.080282; CAB45893.1; -. EMBL; AL.161554; CAB79098.1; -.
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Bost Local Similarity 71.4%;
Matches 5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein;
SEQUENCE 591 AA; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana.
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2; Indels PRT; 1380 AA. 0; Mismatches STANDARD; 122 KFGPKWR 128 1 KFXPXWR 7 ŝ

01-JUN-1994 (Rcl. 29, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOSPHOLIPASE DI (EC 3.1.4.4) (PLD I) (CHOLINE PHOSPHATASE
I) (PHOSPHATIDATICHOLINE-HYDNOLYZING PHOSPHOLIPASE DI) (MEIOSIS-SPECIFIC SPORULATION PROTEIN SPO14). SP14_YEAST P36126; 

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MEDLINE-96161959; Pubmed-8576189;
Waksman M., Eli Y., Liscovitch M., Gerst J.E.;
"Identification and characterization of a gene encoding phospholipase D activity in yeast.";
J. Biol. Chem. 271:2364(1996).
J. Biol. Chem. 271:2361-2364(1996).
J. Biol. Chem. 271:2361-2364(1996).
J. Biol. Chem. 271:2361-2364(1996).
J. Biol. Chem. 271:2363-2364
J. Biol. Chem. 271:2364
J. Beens To BE
ACTIVITY IS INDUCED UNDER SPORULATION CONDITIONS AND SEEMS TO BE
NECESSARY TO COMPLETE THE MEIOTIC CYCLE, BUT NOT FOR VEGETATIVE -i- ENZYME REGULATION: ACTIVITY IS DEPENDENT OF PHOSPHATIDYLINOSITOL. 4.5-BISPHOSPHATE. INHTBITED BY MAGNESTUM.
-i-SIMILARITY: BELONGS TO THE PHOSPHOLIPASE D FAMILY. STRONG, TO S.PONDE SPAC2F7.16C. .i . CATALYTIC ACTIVITY: A PHOSPHATIDYLCHOLINE + H(2)O - CHOLINE + A Hunigberg S.M., Conicella C., Espositio R.E.; *Commitment to meiosis in Saccharomyces cerevisiae: involvement of Enkaryota; Fungl; Ascomycota; Saccharomycotina; Saccharomyceles; Saccharomycetales; Saccharomycetales; WiRI_TaxID=4912; MRDLINE=96109223; PubMed=8618862;
Rose K., Rudge S.A., Frohman M.A., Morris A.J., Engebrecht J.;
Phospholipase D signaling is essential for melosis.";
Proc. Natl. Acad. Sci. U.S.A. 92:12151-12155(1995). 594C48DCA707A3DB CRC64; Jerostarazu L.A., Jauniaux J.-C.; Jubmitted (MAR-1994) to the EMBL/GenBank/DDBJ databases Sporulation; Melosis. POLY-ASN. Saccharomyces cerevisiae (Baker's yeast). or send an email to license@isb-sib.ch). POLY-LEU EMBL: Z28256; CAA82103.1; ALT_INIT. EMBL: L46807; AAA74938.1; -. MEDI,INE-92258685; PubMed-1582554; Hydrolase; Lipid degradation; 160994 Genetics 130:703-716(1992). CHARACTERIZATION AS A PLD unterPro; LPR001849; PH. interPro; LPR001736; PLD PLG"; PF00614; PLDC; 2. SMART; SM00233; PH; 1. SMART; SM00155; PLDC; 2. inturpro; IPR001683; PX 107 SNART; SM00312; PX; 1. SG0: S0001739; SP014 325 3; 1380 AA; PIR; S38103; S38103 P06876; 1MBF PHOSPHAT LDATE. SEQUENCE FROM N.A. CELL GROWTH. the SPO14 gene SHOUENCE NI PROC RSSP; 

ë Gaps : : Score 30; DB 1; Length 1380; Pred. No. 1.6e+02; 1; Mismatches 2; Indels 83.3%; 57.1%; Best Local Similarity 57.1 Matches '4; Conservative I KFXPXWR 7 Query Match ö

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HYPOTHETICAL 16.7 KDA PROTEIN.
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57.1%;
                                                                                                                                                                                                                                                                       Ffam; PF00799; Gemini_AL1;
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Best ideal Similarity 57.10
Since 4: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   May B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                       || | |:
68 KFVPLWK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
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F45524;
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                                                                                                                                                                                                    Miki F., Shimanuki M., Okazaki K., Niwa O.;
"Role of TCTEX-1 like dynein light chain for the function of telomere
associated spindle pole body in fission yeast.";
Submitted (OCT-1999) to the EMBL/GenHank/DDBJ databases.
                                                                                                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 29; DB 1; Length 85; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                            ULC2 OK SPAC926.07C.
Schlzosaccharomyces pombe (Fission yeast).
Bukaryota; Füngl; Ascomycota; Schlzosaccharomycetes;
Schlzosaccharomycetales; Schlzosaccharomycetaceae;
Schlzosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pram: PF01221; Dynein_1ight; 1.
Probom: PP065145; Dynein_1ight; 1.
PROSITE; PS01239; DYNEIN_LIGHT[1: 1.
PROSTE; PS01239; DYNEIN_LIGHT[1: 1.
SEQUENCE: 85 AA; 9822 MW; 81B5EC20081D628A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HESHLF 7
Y17K_TYDVA
AC P31618;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DYNEIN LIGHT CHAIN 1, CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001372; Dynein_light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF197476; AAF05842.1; -. EMBL; AL110469; CAB54155.1; -.
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                                                   S'FANDARD;
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Best Local Similarity
                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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 924 KFSPQWK 930
                                                                                                                                                               NCBI_TaxID-4896;
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                                                 DYL1_SCHPO
09UR05;
                                                                                                                                                                                                                                                                   STRAIN-972;
                                                                                                                                                                                            STRAIN-972;
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                             RESULT 6
DYL1_SCHPO
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STRAIN=KIZ / MG1655;
MEFLINE=97426617; PubMed-9278503;
BLAtther F. R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Hiley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                   SECUENCE FROM N.A.

WEDLINE-92188538; Pubmed-1546458;

MORTIS B.A.M., RICHARGSON K.A., Haley A., Zhan X., Thomas J.E.;

MORTIS B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious choned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coli K-12."; Sclence 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 AA; 16743 MW; 9C8B3C87508D01.0A CRC64;
Tobacco yellow dwarf virus (strain Australia) (TYDV).
Vicuses; ssDNA viruses; Geminiviridae; Mastrevirus.
NCBL_TaxID=31599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : SIMILARITY: BELONGS TO THE UPFOOL7 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                          .! FUNCTION: MAY BE INVOLVED IN REPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN YHET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 AA
                                                                                                                                                                                                                                                                                                                                                                  infecting monocotyledonous plants."; visclogy 187:633-642(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: M81103; AAA47949.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro, IPR001191, Gemini_AL1.
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DN. replication.
SEDUENCE 146 AA; 16743 MW. or
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea: Drosophilidae; Drosophila
NCBI_TaxID*7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                               pram; pr00561; abhydrolase; 1.
PROSTRE: PS01133; UPF0017; 1.
Hypothetical protein: Transmembrane; Complete proteome.
TRANSMEM 147 164 POTENTIAL.
                                                                                                                                                                                                                                                                                                                   7DB6BA6795CBA64D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Last annotation update)
                                                                               EcoGene; EG12904; yher.
InterPro; IPR0000073; Abhydrolase.
IntcrPro; IPR0000739; Est_lip_thioest_actsite.
InterPro; IPR000952; UPF0017.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                           Score 29; DB Pred. No. 70; 1; Mismatches
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PROSITE; PS00193; CYTOCHROME_H_OO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-88212147; PubMed-3130291;
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Pfam: PF00032; cytochrome_b_C: 1.
Pfam: PF00033; cytochrome_b_N: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M37275; AAA69714.1; -. EMHL; 0137541; AAC47822.1; -. PIFR; SOI190; SOI190; FlyBasc; PHGNOO13678; mt:Cyt-b.
                     EMBL; U18997; AAA58150.1; -. EMBL; AE000411; AAC76378.1; -.
                                                                                                                                                                                                                                                                                                                   340 AA; 38495 MW;
                                                                                                                                                                                                                                                                                                                                                                                                        h 80.6%;
Similarity 57.1%;
4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MT:CYT-B OR COB OR CYTB.
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
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SEQUENCE FROM N.A.
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P18935:
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15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updatc)
SELENIDE,WATER DIKINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2)
                                                                                                                                                                                                                                                                                          Gaps
Efection transport, Mitochondrion, Respiratory chain, Transmembrane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- COPACYOR: SELENOCYSTEINE, THE ACTIVE-SITE SELENOCYSTEINE IS ENCODED BY THE OPAL CODON, UGA.

! SIMILARITY: BELONGS TO THE SELENOPHOSPHATE SYNTHETASE 1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and archaea: is there an autoregulatory mechanism in selenocysteine metabolism?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guimaraes M.J., Bazan J.F., Zlotnik A., Wiles M.V., Grimaldi J.C., Lee F., McClanahan T.:
A new approach to the study of haematopoietic development in the valk sac and embryoid bodies.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Galmaraes M.J., Peterson D., Vicari A., Cocks B.C., Copeland N.G., Gilbert D.J., Jenkins N.A., Ferrick D.A., Kastelein R., Bazan J.F., Zholnik A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Futeleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCH:_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'identification of a novel selD homolog from eukaryotes, bacteria
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                                            IRON 1 (HEME B562 AXIAL LIGAND).
IRON 2 (HEME B566 AXIAL LIGAND).
IRON 2 (HEME B562 AXIAL LIGAND).
IRON 1 (HEME B566 AXIAL LIGAND).
6CB9067643ABCEB3 CRC64;
                                                                                                                                                                                                                                     Score 29; DB 1; Length 378 Pred. No. 77;
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(nterPro: IPR000728; AIRS_related.
o'am; PF00586; AIRS: 1.
Norsterase; Selenium; Selenocysteine; ATP-binding.
ACT: STTE 63 63 63
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Development 121:3335-3346(1995)
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98 IR
183 IR
197 IR
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Best Mocal Similarity
                                                                                                                                                      378 AA;
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P97364;
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CONFLICT
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IMPORTANT FOR CATALYTIC ACTIVITY (BY
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Pred. No. 95;
0; Mismatches 2; Indels
                                                                                   Score 29; DB 1; Length 452;
Pred. No. 91;
0: Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome.
SEQUENCE 477 AA; 54041 MW; 81F689981A6D613C CRC64;
                                                   9DA6F7250CFE80E4 CRC64;
                                                                                                                                                                                                                                                                                         Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBI_TaxID•1148;
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Last annotation update)
                      ATP (PUTENTIAL)
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            SIMIL'ARITY)
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                                          POLY - ALA
                               POLY-ALA
                                                                                                                                                                                                                                                                                 Synechocystis sp. (strain PCC 6803).
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MEDLINE~97061201; Pubmed~8905231;
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                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
                                                      47786 MW;
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                                                                                            Local Similarity 66.7
nes 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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P73436;
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P37898;
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Best Local S
Matches 4
                                          DOMAIN
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 265:2077-2082(1994).
-!- FUNCTION: POSITIVE EFFECTOR OF GLYCOGEN ACCUMULATION. MAY BE INVOLVED IN UUTRIENT-SENSING.
-!- COFACTOR: BINDS ONE 21MC ION.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1 (ZINC METALLOPROTEASE);
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STAIN-S286C / A8972;
MEDIAL NE-S286C / A8972;
MEDIAL NE-S4378003; Pubmed-8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Johnston M., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
Vignari D., Wilson R., Waterston R., Wilson R.,
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                                                                               Saccharomyces cerevisiae (Baker's yeast).
Sakaryota: Fungi; Ascomycota: Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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ZINC (CATALYTIC) (BY SIMILARITY).
PROTON DONOR (POTENTIAL).
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SEQUENCE OF 107-652 FROM N.A.
MEDLINE-93300827; Pubmed-8100228;
MEDLINE-93300827; Pubmed-8100228;
Caprioglio D.R., Padilla C., Werner-Washburne M.;
"Isolation and characterization of AAPI. A gene encoding an alanine/arginine aminopeptidase in yeast.";
J. Hiol. Chem. 268:14310-14315(1993).
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Pred. No. 1.6e+02;
1; Mismatches 2; Indels
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0209F9E029BDF9DB CRC64;
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PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Aminopeptidase; Zinc.
01-NOV-1995 (Rel. 32, Last annotation update) ALANINE/ARGININE AMINOPEPTIDASE (EC 3.4.11.-)
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MARL; U000062; AAB68919.1; -
PIR; S46750; S46750.
MEXOPS; M01.007; -
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Accervo: PR001930; Aladiptase.
InterPro: IPR00130; Zn_WTpeptdse.
Pfam: PF01433; Peptidase_M1: 1.
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Similarity 57.1%;
4; Conservative
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                                                              AAP1 OR YHR047C
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6 FSPLWR 11
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C86110;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Hioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Narberhaus F., Weiglloder W., Fischer H.M., Hennecke H.,
"Identification of the Bradyrhizobium japonicum degP gene as part
an operon containing small heat shock protein genes.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-:- STMILARITY: HELONGS TO THE SWALL HEAT SHOCK PROTEIN (HSP20)
FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                            MEDLINE-88219532: PubMcd-3369088;
Andersen M.T., Richardson K.A., Harbison S.A., Morris B.A.M.;
"Nucleotide sequence of the qeminivirus chloris striale mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.8%; Score 28; DB 1; Length 136; 57.1%; Pred, No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15762 MW; C320AFD34F811C55 CRC64;
                                                     01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last, Sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
HYPOTHETICAL 15.8 KIAA PROTEIN.
Chloris striate mosaic virus (CSMV).
Viruses; SSDNA viruses; Geminiviridae; Mastrevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last Sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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                  136 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobium group; Bradyrhizobium.
NCBI_TaxID-375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M20021; -; NOT_ANNOTATED_CDS.
PIR; JU0044; JU0044.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00799; Gemini_ALI; I.
Probom: PD00736; Gemini_ALI; 1.
Hypothetical protein
SEQUENCE 136 AA: 15762 MW; C
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                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best, Local Similarity
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                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID-10820;
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62 KFVPCWK 68
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                  Y16K_CSMV
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HSPD_BRAJA
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INT 30-MAY
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial suities requires a license agreement (See http://www.isb-sib.ch/announce/or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myenchbach M., Nocker A., Narberhaus F.;
"Occurrence of a superfamily of small heat shock proleins in
Bradyrhizobium japonicum and other Rhizobium species: a plant-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3radyrhizobium japonicum.
Barieria: Proleobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group: Bradyrhizobium.
NCSI_TaxID-375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-1998) to the EMBL/GenHank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                  1; Length 151;
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                                                                                                                                                                                                                                                                           Hea: shock: Multigene family.
SEQUENCE 151 AA; 17272 MW;. FB44EF94FB599EE4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
PI-MAY-2000 (Rel. 39, Last sequence update)
RP-EAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                            Score 28; DB
Pred. No. 53;
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0; Mismatches
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66.7%; Pred. No.
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PF00011; HSP20; 1.
                                                                                                                                                        9781: AJ003064; CAA05835.1; -. 3.82.7Pro; IP3002068; Crystallin_HSP20.
Přam; PF00011; HSP20; 1.
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                                                                                                                                                                                                                                                                                                                                                                                               77.8%;
66.7%;
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Genfore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	<pre>protein search, using sw mode!    February 27, 2002, 11:54:08 ; Search time 62.61 Seconds    (without alignments)    16.354 Million cell updales/sec</pre>	US-09-446-109A-24 C:36 1 KFXPXWR 7 e: BLOSUM62 Gapop 10.0 , GapexL 0.5	Searched: 473505 seqs, 146272329 residues Total number of hits satisfying chosen parameters: 473505	eq length: 0 eq length: 200000000	iing: Minimum Match 0% Maximum Match 100% Listing Lirst 45 summaries	SPTREMHL_17:*  1: sp_archea:* 2: sp_baccerla:* 3: sp_tungi:* 4: sp_human:* 5: sp_human:* 7: sp_mn = 1:* 7: sp_mn = 1:* 8: sp_organelle:* 9: sp_phage:* 10: sp_plant:* 11: sp_ordent:* 12: sp_virus:* 13: sp_vertebrate:* 14: sp_unclassified:*
Copyr	OM protein - protein se Kun on: Februa	Title: US-09-09-09-09-09-09-09-09-09-09-09-09-09-	Searched: 473505 Total number of hits sa	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match U% Maximum Malch 10 Listing lirst 45	<u>7</u>

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sucsophila melanogaster (Fruit ily).
Sukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Sucryota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Subydroidea; Drosophilidae; Drosophila.

\$00AIN=BERKELEY; MED.INE=20196006; Pubmed=10731132;

SOUTH BUCK FROM N.A.

			Description	Q9vld3 drosophila	Q9eum2 corynebacte	Q84836 potato leaf	Q9f756 bacteroldes	Q57935 methanococc	023080 arabidopsis	Q9fkv6 arabidopsis	Q99h27 heliocoverp	Q9ybb9 aeropyrum p	Q67622 wheat dwarf	Q9m7w6 arabidopsis	Q9fle6 acetobacter	. O91si4 arabidopsis	080627 arabidopsis	Q910k8 pseudomonas	Q9aa59 caulobacter	Q9a313 caulobacter	O9n889 plasmodium	Q9dsv9 ascovirus d
SUMMARIES			ID	09VLD3	Q9EUM2	084836	Q9F756	057935	023080	09FKV6	Q99H27	Q9YBB9	067622	09M7W6	09F1E6	091.514	080627	Q910K8	Q9AA59	094313	688N6O	690509
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			Score	33	33	33	32	32	32	32	32	31	30	30	30	30	30	30	30	30	30	57
		Result	Q	-	7	3	7	ທ	9	7	90	6	10	11	12	13	7	15	16	17	18	19

Activity—100-50 (1960) by Dubmod-10/31132, AGGININE-20160006, Pubmod-10/31132, AGGININE-20160006, Pubmod-10/31132, AGGININE-20160006, Pubmod-10/31132, ASHURINE-2016006, ASHURINE S.E., Holf P.W., Hoskins R.A., Galle R.E., ASHURINE S.E., Richards S., Ashurine M., Hentferson S.N., ASHURINE G.G., Champe M., Pfelffer B.D., ASHURINE C., Bazer E.G., Helt G., Nelson C.R., Milklos G.L.G., ASHURINE S.E., Barcas P.P., Daylos C.R., Alliklos G.L.G., Barcher E.G., Helt G., Nelson C.R., Milklos G.L.G., Ashuri L.F., Ashuayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., R.A., Ashuri K.Y., Bencas P.V., Berman B.P., Bhandadari D., Bostete P., Bardakov S., Ashuri K.Y., Bencas P.V., Berman B.P., Bhandadari D., Bostete P., Bottler P., Harris M., Golde R., Golg F., Gorrell J.H., Gu Z., Guan P., Harris M., Ashush P., Howland T.J., Woll M.-H., Ibogwam C., Ashush P., Lill M., Kallush P., Karben G.H., Ke Z., Kennison J.A., Ketchum K.A., Ashush P., Levils Y., Ashush P., Lin X., Matteri B., McJintosh T.C., McLeod M.P., Moshrefi A., Aderkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Aderkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

	20 . 29	90.6	1.22	7	O9K0W8	Q9k0w8 ncisseria n.
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	25. 29	80.6	157	11	Q9CR22	Q9cr22 mus musculu
			204	Ξ	Q903F2	2
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	2		239		Q9B399	Q9b399 blackburnia
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1 KFXPXWR 7
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Relazalo M., Pitlman G.S., Pan S., Pollard J., Parleb J.M.,
A Palazalo M., Pitlman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Syliskas K., "Getor C., Turner R., Wonter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Wolnstock G.M., Weissenbach J.,
A Wang Z.-Y., Wassarman D.A., Wolnstock G.M., Weissenbach J.,
A Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
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A Zheng X.H., Apers E.W., Rubin G.M., Venter J.C.,
"The genemic sequence of Drosophila melanogaster.",
Science 287:2185-2195(2000).
BEMBL, AE003644, AAF52799.1;
SEMBL, AE003644, AAF52799.1;
SEQUENCE 241 AA; 27071 MW; 200925FE35G3F33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tauch A., Puehler A., Kallnowski J.;
DNA sequence and genetic organization of the integron-carrying R-plasmid pCG4 of Corynebacterium glutamicum.";
Submitted (JUL-1999) to the EMBL/GcnBank/DDBJ databases.
BML. AFG4956, AAG00294.1;
InterPro: IPR002145; CopG_HTH_4.
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Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales: Corynebacterineae: Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AA; 28804 MW; 195C86367H483157 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum (Brevibacterium flavum).
Plasmid R.plasmid pCG4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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(TrEMBLrel. 01, Last seq
(TrEMBLrel. 17, Last anno
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71.48;
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71.48;
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Best Local Similarity 71.4
Matches 5; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-ATCC31830;
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213 KFKPAWR 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCH [_Tax ID-1718;
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67 KETPVWR 73
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01-JUN-2001
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SEQUENCE
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Q84836;
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Q84836
ID Q8
AC Q8
DT 01
DT 01
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"Bacteroides fragilis NCTC9343 Produces at Least Three Distinct
Capsular Polysaccharides: Cloning, Characterization, and Reassignment
of Polysaccharide B and C Hiosynthesis Loci.";
Infect. Immun. 68:6176-6181(2000).
EMBL: AF285774, AAG26474.1:
InterPro: IPR001173; Glycos_transf_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Potato leafroll virus (PLrV).
VIruses: ssRNA positive-strand viruses, no DNA staye; Luteoviridae;
Polerovirus.
                                                                                                                                                                                        Palucha A., Sadowy E., Kujawa A., Juszczuk M., Zagorski W.,
Mulanicka D.;
Nuclectide sequence of RNA of a Polish isolate of potato leafroll
luteovirus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Darteroldes fragilis.
Barteria: CFB group: Bacteroldaceae: Bacteroldes.
NCHL_TaxID=817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 12; L
Pred. No. 1.1e+02;
0; Mismatches 2;
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Last sequence update)
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MEDLINE=20490546; Pubmed=11035722;
                                                                                                                                                                  MEDLINE=95250405; PubMed-7732757;
                                                                                                                                                                                                                                                                                                     EMBL; X74789; CAA52790.1; -...
(InterPro: IPR000382; Luteo_ORF2.Pfan: PF02122; Luteo_ORF2.1.PRINVS; PR00913; LVTRUSORF2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.78;
71.48;
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Q57935;
01-JAN-1998 (TrEMBLREL 05, 01-JAN-1998 (TREMBLREL 05,
                                                                                                                  SEQUENCE FROM N.A.
STRAIN-THE POLISH ISOLATE;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.4.
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Matches 5; Conserv
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                                                                      NCBI_TaxID-12045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             514 KFIPSWR 620
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299 KFLPYWR 305
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STRAIN-CV. COLUMBIA;
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Q99H27
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SO OR 
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O
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-i- COFACTOR: NICKEL (HY S[HILARITY).
-i- PATHWAY: HYDROGEN WETABOLISM: FHL. PATHWAY (BY SIMILARITY).
-i- SUBUNIT: FHL. COMPRISES OF A FORMATE DEHYDROGENASE, UNLDENTIFLED
--- SUBUNIT: FHL. COMPRISES AND A HYDROGENASE (ISOENZYME 3). IN THIS NON-
--- EMEGY CONSERVING PATHMAY WOLECULAR HYDROGEN AND CARBODIOXIDE FROM
--- FORMATE ARE RELEASED (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE COMPLEX I 49 KDA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                               STRAIN-JAL-1 / DSW 2661 / ATCC 43067;
STRAIN-JAL-1 / DSW 2661 / ATCC 43067;
BUIL C.J., White O., Oisen G.J., Zhou L., Fleischmann R.D.,
BUIL C.J., White O., Oisen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Soutcheek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback R., Kolley J.M., Peterson J.D., Sadow P.M., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.,
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermalophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
01-JUN-2001 ("rEMBLICEL. 17, Last annotation update)
PUTATIVE FORMATE HYDROGENLYASE SUBUNIT 5 (FHL SUBUNIT 5) (HYDROGENASE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00535; COMPLEXI 49K; UNKNOWN 1.
PROSITE; PS00507; NL HGFNASK_I._1: UNKNOWN_1.
Hypothetical protein; Oxidoreductase; NAD; Iron-sulfur; 4Fe-4S;
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                                                                                                                                          Methanococcus jannaschii.
Archaea: Euryarchaeota; Methanococcales; Methanococcaceae;
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Pred. No. 1.ie+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dempsey S., Harper M.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43638 MW; 3EAD16D67834A76F CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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A_TM018A10.1 OR AT4G00980.
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InterPro; IPR001051, NIFESS_Hases.
Pfam; PF00346; Complex1_49kd; 1.
Pfam; PF00374; NIFESS_Hases; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 273:1058-1073(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U67501; AAB98504.1;
TIGR; MJ0515; -.
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240 KFKPVWR 246
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Eskaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Suermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; escosids II; Brassicales; Brassicaceae; Arabidopsis.
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Кавско Т., Kotani II., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
Fabata S.;
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DNA Res. 5.13-146(1998).
EMBL: AB011475; BAB10117.1;
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Waterston R.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                 Railonitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462 AA; 52052 MW; C4A12045D0376E33 CRC64;
                                                                                                                                                                                                    Off Arabidopsis sequencing project;
%Johntted (MAR-2000) to the EMBL/GenBank/DDBJ database
%-SIMILANTITY: BELONGS TO ZN-FINGER CCHC TYPE FAMILY
6MBL; AF013294; AAB62847.1; --
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
EUXARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 7.
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Pred. No. 1.6e+02;
0; Mismatches 2;
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                                                                                      T., Stumpf J., Mewes
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PRINTS; PR00939; C2HCZNFINGER.
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milarity 71.4%;
Conservative 0
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Bos Local Similarity
Fos 5; Conserve
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Fekaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliephyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCRI_TaxID-3702;
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosuqi H., Hosoyama A., Fukui S., Nagai Y., Nishljima K., Nakazawa II., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; "Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
MacDowell S.W., MacDonald H., Hamilton W.D.O., Coutts R.H.A.,
MacK K.W.;
EMBO J. 4:2173-2180(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.3%; Score 30; DB 12; Length L50;
57.1%; Pred. No. 1.1e+02;
Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                              Length 254;
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InterPro: IPR001191; Gemini_ALI.
Fram. PF00799; Gemini_ALI.1; I.
Erobom: PD000736; Gemini_ALI.1; 1.
SECUENCE 150 AA: 17292 MW; 3B7394DCB793F9FB CRC64;
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D173589517FD0D2A CRC64;
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Last annotation update)
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Viruses: ssDNA viruses: Geminiviridae; Mastrevirus.
NCBL_TaxID=10834;
                                                                                                                                                                                                                                                          Score 31; DB 1; Le
Pred. No. 1.2e+02;
1; Mismatches 2;
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                                                                                                                   crenarchaeon, Aeropyrum pernix Ki.";
DNA Res. 6:83-101(1999).
EMBL. AP000062; BAA80679.1; -.
HY:Othetical protein; Complete proteo
SEQUENCE 254 AA; 27026 MW; D17358
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Best focal Similarity 57.1%;
Match@s 4; Conservative
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65 KFTPNWK 71
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"Sequence analysis of the ap37 gene of Heliothis armigera single-
nucleocapsid nucleopolyhedrovirus.";
chongguo Bingduxue 15:35-42(2000).
                                                                                                                                                                                                                                                                                                                                                Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;
Sedeuche analysis of the lap3 gene of Heliothis armigera single-
nucleocapsid nucleopolyhedrovirus.",
Zhongguo Bingduxue 15:43-49(2000).
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MEDLINE÷99310339; Pubmed-10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
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J. Gen. Virol. 82:241-257(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 688;
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                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                     01-JUN-2001 (TTEMHLICI. 17, Last sequence update)
01-JUN-2001 (TTEMHLICI. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-3UN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHERICAL 27.0 KNA PROPEIN APPLE78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heliocoverpa armigera nucleopolyhedrovirus G4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 AA
                                    (TrEMBLiel, 17, Created) (TrEMBLiel, 17, Last Seq.
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  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17,
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                   Nucleopolyhedrovirus.
NCBI_TaxID-148363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed-11125177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 | ||
49 KFIPKWR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KFXPXWR 7
                                    01-JUN-2001
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                  299H27;
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"Structural analysis of Arabidopsis thallana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC clunes.";

Charles.";

FMBL, AB026645; BAB02498.1;

FMBL, AP000385; BAB02498.1;

FMBL, AP000385; BAB02498.1;
                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eur:sids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eskaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae: Pricosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schooley S.D. Lin X., Ketchum K.A., Crosby M.L., Brandon R.C., Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D., Shenville C.R., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=COLUMBIA;
Sato S., Nakamura Y., Kancko T., Kato T., Asamizu E., Tabata
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30; DB 10; Length 31. Prod. No. 2.26+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%; Score 30; DB 10; Length 30
57.1%; Pred. No. 2.1e+02;
ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ChterPro: IPR000073; Abhydrolase.
ChterPro: IPR000379; Est_lip_thioest_actsite.
Pram: PF00561; abhydrolase; 1.
SROJENCE 317 AA; 35937 MW; E6429D3BD07FDCHE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Priam: PF02365; NAM; 1. FP77F62358BDECC CRC64; FF30ENCE 303 AA; 35198 MW; FDF77F62358BDECC CRC64;
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08, Last sequence update)
17, Last annotation update)
                                 0):OCT-2000 ("remBirel. 15, Created)
01-OCT-2000 (TrEMBirel. 15, Last sequence update)
01-UN-2001 (TEMBirel. 17, Last annotation update)
33M:LATTY TO NAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN~COLUMBIA;
MEDLINE~20277480; Pubmed=10819329;
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Rest Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, 91-NOV-1998 (TrEMBLrel. 08, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, AC004218; AAC27831.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003441; NAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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|91. KYTPDWR 197
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MEDILINE-20545459.
Lee S., Reth A., Meletzus D., Sevilla M., Kennedy C.;
Lee S., Reth A., Meletzus D., Sevilla M., Kennedy C.;
Lee S., Reth A., Mclostus D., Sevilla M., Kennedy C.;
Lee S., Reth A., McGastus D., Sevilla M., Kennedy C.;
J. Bacteriol of McGastus D., Secondard Cenes
J. Bacteriol. 182:7088-7091(2000).
J. Bacteriol. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis tha lana chromosome III Pl MGH6 genomic sequence."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ACC024128; AAR53540.1; - SEQUENCE 160 AA; 18620 MW; 95651977DE161826 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acetobacter diazotrophicus.
Bacteria; Proleobacteria; alpha subdivision; Acetobacteraceae;
Gluconacetobacter.
NCBI_TaxID+33996;
                                                                                                                                                                                                                                                  DB 10; Length 160;
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Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                          DB 1.2e+02;
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                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                  Score 30;
Pred, No. 1
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nilarity 57.1%;
Conservative
                                                                                                                                                                                                                                               Ouery Match 83.3%;
Best Local Similarity 57.1%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Matches 4: Conserv
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72 REVPAWR 78
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48 KYTPIJWR 54
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SEQUENCE FROW N.A.

STAIN-PAOJ;
WATIN-PAOJ;
WEDLINE-20437337; PubMed-10984043;
MEDLINE-20437337; PubMed-10984043;
MEDLINE-20437337; PubMed-10984043;
MEDLINE-20437337; PubMed-10984043;
MA HCKey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., A Garber R.L., Coulter S.W., Tolontino E., Westbrock-Wadman S., Yuan Y., RA Brody L.L., Coulter S.W., Folontino E., Wustbrock-Wadman S., Yuan Y., RA Brody L.L., Saler M.H., Hancock R.E.W., Lory S., Olson M.V., Razer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V., Razer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V., RT Complete genome sequence of Pseudomonas aeruginosa PAOJ, an opportunistic pathogen.";
Nature 406:959-964(2000).

REMBL, AED004691; AAG06018.1;
REMBL, AED004691; AAG06018.1;
SEQUENCE 389 AA: 44057 MW: 10FFBC62E92467C7 CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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Search completed: February 27, 2002, 11:54:09 Job time: 229 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-795-445A-6
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US-09-795-425-1
US-09-153-927-1
US-09-153-927-1
US-09-1091-219-25
US-09-091-219-25
US-09-091-219-25
US-09-216-137-13
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APPLICANT: BOYLE, Willaim J. APPLICANT: Calzone, Frank J. APPLICANT: Calzone, Frank J. TETER OF INVENTION: OSTEOPROTEGERIN NAMMER OF SEQUENCES: 53 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5426049-1
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COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER:
INCHMATION FOR SEQ ID NO: 6
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STATE: California
COUNTRY: USA
ZIP: 91320-1789
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Gaps

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Score 28; DB 3; Length 401; pred. No: 2.1e+02; 0; Mismalches 2; Indels

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SUPPLIER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentr Polician
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                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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                                                  Sequence 12, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICATOR Husfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TIME RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28; DB 4; I
Pred. No. 2.1e+02;
0; Mismatches 2;
                                                                                                                                                                                                ADDRESSEE: LAHIVE & COCKFLELD, LLP
STREET: 20 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mandragouras, Amy E
HEGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-MAK-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lacey, was an APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/08795445A
Patent No. 6284485
GENERAL INFORMATION:
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1840 Dehavilland Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617)227-7400
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amino acid
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INFORMATION FOR SEG ID NO:
SEQUENCE CHARACTERISTICS:
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internal
                                                                                                                                                                NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc
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CITY: Thousand Oaks
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Best Local Similarity
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                                                                                                                                                                                                                                                                           USA
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FRAGMENT TYPE:
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                                 US-09-042-785A-12
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Gaps
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Pred. No. 2.1e+02;
0; Mismatches 2; Indels
SOFTWARE: Patentin Ralease #1.0, Version #1.30 CGRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
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Pred. No. 2.1e+02;
                                           APPLICATION NUMBER: US/08/795,445A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08795447A Patent No. 628472B CENESAL, INFORMATION:
APPLICANT: BOYLE, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: One Amgen Center Drive CITY: Thousand Oaks STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boyle, William J.
Lacey, David L.
                                                                                                                                                                                                                TYPE: amino acids
TOPOLOGY: lin-
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66.7%;
                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: MAME: Winter, Robert B. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 401 amino acids
amino acid
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Best Local Similarity
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Matches

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GENERAL INFORMATION:
APPLICANT: WCDONNell, Peter C.
APPLICANT: WCDONNell, Peter C.
APPLICANT: YOU, JUN
TILLS OF INVENTION: A Method of Identifying Agonists and
TITLS OF INVENTION: Antagonists for Tumor Necrosis Related Receptors Tkl, TR3
TITLS OF INVENTION: and TR5
FILE REFERENCE: GH50031
CURRENC APPLICATION NUMBER: US/09/153,927A
CURRENC FILING DATE: 1998-09-16
EARLIER FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 11
SOGWWARE: PASLSKQ for Windows Version 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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66.7%; Pred. No. 2.1e+02;
ive 0; Mismatches 2; Indels
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Pred, No. 2.1e+02;
                                                                                                         SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30
                                                                                                                                          CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/795,446B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09153927A Patent No. 6297022
                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                        NAME: WINTER, ROBEL B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 6
SUGENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                            ACTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 401 amino acids TYPE: amino acid
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Best Local Similarity 66...
New 4; Conservative
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MALECULE TYPE: protein

US-08-795-4468-6
California
                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
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Best focal Similarity
Matches 4; conserv
                                 91320-1789
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214 KETPNW 219
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- ORUANISM: Human
US-09-153-927-1
                                                                                                                                                                                                                                                             FILING DATE:
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Pred. No. 2.1e+02;
0; Mismatches 2; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
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Mismatches
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APPLICANT: Hoyle, Willaim J.
APPLICANT: Lacey, David f.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
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APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTECRIN
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                               STREET: Amgen inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
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1840 Dehavilland Drive
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
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; Patent No. 6284740
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NAME: Winter, Robert B.
REFERENCE/FORET UNBER: INFORMATION FOR SEQ ID NO: 6:
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amino acid
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Best Local Similarity 66.77
Local 4; Conservative
4; Conservative
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ZIP: 91320-1789
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                                                                        214 KFTPNW 219
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                                   1 KFXPXW 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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APPLICANT: Konteatis, Zenon APPLICANT: Siciliano, Salvatore J APPLICANT: Siciliano, Salvatore J APPLICANT: Springer, Martin S TITLE OF INVENTION: ASSAY TO IDENTIFY HUMAN C5A ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB 4; Length 2232;
Pred. No. 1.1e+03;
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                  APPLICANT: CRABB, Hrendan S.
APPLICANT: CRABB, Hrendan S.
APPLICANT: FENG, Li.
TITLE. DE INVENTION: EQUINE RHINOVIRUS I PROTEINS
FILE REFERENCE: 040268/0151
CURENT APPLICATION NUMBER: US/09/091,219
CURENT APPLICATION NUMBER: US/09/091,219
CURENT APPLICATION NUMBER: PCT/AU96/00815
EAX.IER APPLICATION NUMBER: PCT/AU96/00815
EAX.IER APPLICATION NUMBER: AU PN7201
EARLIER FILING DATE: 1995-12-18
SEALIER FILING DATE: 1995-12-18
SOFTWARE PERGIN VOR. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STODERT, Michael J.
APPLICANT: STODERT, Michael J.
APPLICANT: STODERT, Michael J.
APPLICANT: FENG, Li.
APPLICANT: FENG, Li.
TITLE OF INVENTION: EQUINE RHINOVIRUS | PROFILE STILE REFERENCE: 040268/0151
CURRENT APPLICATION NUMBER: US/09/091,219
CURRENT FILING DATE: 1998-10-05
EAPLIER FILING DATE: 1998-12-18
EARLIER FILING DATE: 1995-12-18
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: equine rhinovirus 1
US-09-091-219-25
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Best Local Similarity
Matches 4; Conserv
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Bost Gocal Similarity
Matches 4; Conserv
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1327 FVPTWR 2232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 | 1 | 1 | Db 2227 FVPTWR 2232
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LENGTH: 2247
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US-09-091-219-2
                                                                                                                                                                                                                                                                                                                                                                                                               PRT
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APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or TITLE OF INVENTION: Heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT FILLING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILLING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                     APPLICANT: RILCY, Lee W.

TITLE OF INVENTION: DNA MOLECULE ENCODING FOR CELLULAR UPTAKE OF
TITLE OF INVENTION: MYCHAGTERIUM TUBERCULOSIS AND USES THEREOF
FILE REFERENCE: 19603/1531
CURRENT APPLICATION NUMBER: US/08/907, 229A
CURRENT APPLICATION NUMBER: US/08/907, 229A
CURRENT APPLICATION NUMBER: 60/040,097
EARLIER APPLICATION UNHHER: 60/040,097
NUMBER OF SED 1D NOS: 2
SOFTWARE: PATENTIN UNFILE STORY
LEARLIER APPLICATION UNFINER: 60/040,097
LEARLIER APPLICATION UNFINER: 1997-03-10
SEQ ID NO 2
LENGTH: 5277-
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Pred. No. 7.7e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB 3;
Pred. No. 2.8e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                               . ORGANISM: Mycobacterium tuberculosis US-08-907-229-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Sequence 25, Application US/09091219
; Patent No. 6171592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09413814
Patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Clino, Paul M
APPLICANT: Cloodherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 77.8%;
Best Local Similarity 66.7%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 66.7
Matches 4: Conservative
Patent No. 6072048
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896 FLPAWR 901
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3 FGPSWR 8
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49 ICANT: Stewart, Timothy A. Tim
Length 873;
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Pred. No. 7.1e+02;
0; Mismatches 2; Indels
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JE-08 CHRIST 46-1

Sequence 1, Application US/08392946

Particle 1, Application US/08392946

GRITCH INFORMATION:

CHRIST AND ADMINISTRA OF CHE University of California

CHRIST Soldfine, Ira D.

CHRIST SOLD AND AND ADMINISTRA ADMINIS
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APPLICANT: COTIES, Neil C.
APPLICANT: COMPELY, Karl J.
APPLICANT: GOMENIE, Karl J.
APPLICANT: GOMENIE, Karl J.
APPLICANT: GOMENIE, MARIAH R.
TITULE OF INVENTION: CELL SURFACE GLYCOPROTEINS
TITULE OF INVENTION: CELL SURFACE GLYCOPROTEINS
FILE OF THE PREMERS: PF-0631 US
CUTRENT FILENCIPATE: 1998-11-06
NUMBER OF SEQ ID NOS: 6
NUMBER OF SEQ ID NOS: 6
SEX (O NO 6)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 4;
pred. No. 3.8e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09187331
: Patent, No. 6043056
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Organization 75.0%; But Could Similarity 66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Lonal Similarity 66.7
Manages 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CASSALSM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09 - 67-331-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 4 OTHER INFORMATION: /label- dCha OTHER INFORMATION: /note= "D-cyclohexylalanine"
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: 1HM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACCULIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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OTHER INFORMATION: /note- "D-arginine"
US-08-215-137-13
                                                                                                                                                                                          ADDRESSEE: Merck & Co., Inc.
STREET: 126 Linclon Ave., P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-268-364-21; Sequence 21, Application US/09268364A; Patent No. 6204063
                                                                                                                                                                                                                                                                           CITY: Kahway
STATE: New Jersey
COUNTRY: United States of America
                                                           TITLE OF INVENTION: AND AGONISTS NUMBER OF SEQUENCES: 15 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATORNEY AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: 19108
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3901
TELEPHONE: (908) 594-4720
INFORMATION FOR SEO 1D NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 minn acids
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83.3%;
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APPLICANT: Lee, Jian Ming
APPLICANT: Lightner, Jonathan
APPLICANT: Odell, Joan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
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LOCATION: 1
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NAME/KEY: Modified-site
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Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ID: 94080
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IMP C compatible
OPERATING SYSTEM: CP-705/AS-005
SOFTWARE: Winpalin (Genentech)
COMPUTER: IMP C COMPATIBLE
SOFTWARE: Winpalin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,946
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/08/392,946
FILING DATE: 14-JAH-1994
ATTORNEY/AGENT INFORMATION:
FLECOMMINICATION INFORMATION:
TELEPHIONE: 650/252-9881
INFORMATION FOR SEO I) NO: 1:
SEGUENCE CHARACTERISTICS:
ILENGTH: 925 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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Scarch completed: February 27, 2002, 11:50:38 Job time: 867 sec

1 KFXPXW 6 || | | | |295 KFNPEW 300

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Query Match 75.0%; Score 27; DB 2; Longth 925; Best Local Similarity 66.7%; Pred. No. 7.5e+02; Matches 4; Conservative 0; Mismatches 2; Indels